

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2005, 23:54:06 ; Search time 165 Seconds
(without alignments)
53.912 Million cell updates/sec

Title: US-10-674-065-3

Perfect score: 132

Sequence: 1 ERGPPGPGQARGFGPTGLPGVK 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	23	8	Adn12242 Type II c
2	132	100.0	24	8	Adn12248 Type II c
3	132	100.0	24	8	Adn12245 Type II c
4	132	100.0	24	8	Adn12247 Type II c
5	132	100.0	24	8	Adn12246 Type II c
6	132	100.0	84	8	Adn12240 Type II c
7	132	100.0	84	8	Adn12251 Type II c
8	132	100.0	85	8	Adn12250 Type II c
9	132	100.0	243	8	Adq18267 Human sof
10	132	100.0	1014	7	Adc21544 Human typ
11	132	100.0	1417	8	Abm83560 Human dia
12	132	100.0	1418	2	Aar59751 Type II c
13	132	100.0	1418	2	Aar71703 Collagen
14	132	100.0	1418	3	Aay96124 Collagen
15	132	100.0	1418	4	Aab35624 Human typ
16	132	100.0	1418	5	Aae16477 Human col
17	132	100.0	1418	5	Abbs80735 Collagen
18	132	100.0	1418	5	Abgs93927 Human pol
19	132	100.0	1418	5	Abbo9627 Amino aci
20	132	100.0	1418	7	Adf13077 Human col
21	132	100.0	1420	8	Adp48530 Full-length
22	132	100.0	1487	2	AAw61562 Human typ
23	132	100.0	1487	5	Abg61861 Prostate
24	132	100.0	1487	6	Abp56769 Collagen
25	122	92.4	1014	7	Adc21591 Mouse typ

26	122	92.4	1419	7	AD555694	Ad555694 Rat Prote
27	122	92.4	1487	5	ABG93928	ABG93928 Mouse pol
28	117	88.6	1442	2	AAR79480	AAR79480 Rat type
29	115	87.1	102	4	AAB568055	AAB568055 Amino aci
30	115	87.1	102	4	AAE02701	AAE02701 Human alp
31	115	87.1	102	7	ADB84288	ADB84288 Recombina
32	115	87.1	130	4	ABU53017	ABU53017 Human tes
33	115	87.1	134	4	ABU53021	ABU53021 Human tes
34	115	87.1	154	4	ABU53012	ABU53012 Human tes
35	115	87.1	261	4	AAE02702	AAE02702 Human alp
36	115	87.1	261	7	ADB84289	ADB84289 Recombina
37	115	87.1	294	7	AD587060	AD587060 Human pan
38	115	87.1	310	2	AAY06238	AAY06238 Mouse rec
39	115	87.1	501	4	AAE02703	AAE02703 Human alp
40	115	87.1	501	7	ADB84290	ADB84290 Recombina
41	115	87.1	595	2	AAY06239	AAY06239 Mouse rec
42	115	87.1	614	7	AD587059	AD587059 Human pan
43	115	87.1	615	7	AD587063	AD587063 Human pan
44	115	87.1	691	7	AD587058	AD587058 Human pan
45	115	87.1	822	2	AAY06240	AAY06240 Mouse rec

ALIGNMENTS

RESULT 1

ADN12242

ID ADN12242 standard; peptide; 23 AA.

XX AC ADN12242;

XX DT 01-JUL-2004 (first entry)

XX DE Type II collagen degradation rate altering peptide CB12-II.

XX KW Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
XX KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.

XX OS Synthetic.

XX PN WO2004031206-A2.

XX PD 15-APR-2004.

XX PF 30-SEP-2003; 2003WO-US030744.

XX PR 30-SEP-2002; 2002US-0414332P.

XX (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.

XX PI Poole AR;

XX WPI; 2004-316460/29.

XX DR New peptides that regulate the degradation of type II collagen, useful
XX PT for diagnosing and treating for e.g. osteoarthritis, rheumatoid
XX PT arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or
XX PT eye diseases.

XX Claim 1; Page 50; 74pp; English.

XX The invention relates to an isolated or purified peptide comprising a
XX fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III,
XX CB12-IV, Pro6, Prol5, Prol8 or Pro21, or its fragment, conservatively
XX substituted variant, mimetic, inhibitor or homologue. The peptide alters
XX the rate of degradation of type II collagen or the rate of chondrocyte
XX hypertrophy. The peptide or its fragment is hydroxylated at one or more
XX of the proline or lysine residues of the peptide. A pharmaceutical
XX composition comprising a pharmaceutical carrier and at least one of the
XX peptide inhibitors cited above, is useful for reducing collagen matrix
XX turnover in mammals, particularly humans, or for reducing degradation of
XX one or more collagen proteins. An isolated or purified antibody that
XX specifically binds to an epitope of the peptide or its antigenic fragment

CC is used to inhibit the activity of the peptide, to identify inhibitors of
 CC the generation of the peptide, or to identify a subject at risk for rapid
 CC or slow progression of a disease responding to therapy designed to arrest
 CC cartilage degradation or at risk for a disease by showing of early pre-
 CC clinical changes prior to clinical presentation of the disease, where the
 CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
 CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
 CC addition, the antibody is used to detect the release of type II collagen
 CC degradation products in body fluids, e.g. tissue extracts, serum,
 CC synovial fluid or urine. The composition and methods may be used for
 CC diagnosing and treating such diseases. The present sequence represents a
 CC specific example of the peptide effective in altering the rate of
 CC degradation of type II collagen or the rate of chondrocyte hypertrophy.
 XX
 SQ Sequence 23 AA;

Query Match 100.0%; Score 132; DB 8; Length 23;
 Best Local Similarity 100.0%; Pred. No. 8.5e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ERGPPGPGQARGFGTGTGLPGVK 23
 DB 1 ERGPPGPGQARGFGTGTGLPGVK 23

RESULT 2
 ADN12248
 ID ADN12248 standard; peptide; 24 AA.
 XX
 AC ADN12248;
 XX

01-JUL-2004 (first entry)

Type II collagen degradation rate altering peptide Pro21.

XX Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
 KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.
 XX
 OS Synthetic.

Key Location/Qualifiers
 FT Modified-site 6 /note= "hydroxylated proline"
 FT Modified-site 15 /note= "hydroxylated proline"
 FT Modified-site 18 /note= "hydroxylated proline"
 FT Modified-site 18 /note= "hydroxylated proline"

XX WO2004031206-A2.
 PN
 XX
 XX 15-APR-2004.
 XX
 XX 30-SEP-2003; 2003WO-US030744.
 XX
 XX 30-SEP-2002; 2002US-0414332P.
 XX
 XX (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.

XX Poole AR;

XX WPI; 2004-316460/29.

XX New peptides that regulate the degradation of type II collagen, useful
 PT for diagnosing and treating for e.g. osteoarthritis, rheumatoid
 PT arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or
 PT eye diseases.

XX Claim 1; Page 50; 74pp: English.

XX The invention relates to an isolated or purified peptide comprising a
 CC fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III,
 CC CB12-IV, Pro6, Pro15, Pro18 or Pro21, or its fragment, conservatively
 CC substituted variant, mimetic, inhibitor or homologue. The peptide alters

CC the rate of degradation of type II collagen or the rate of chondrocyte
 CC hypertrophy. The peptide or its fragment is hydroxylated at one or more
 CC of the proline or lysine residues of the peptide. A pharmaceutical
 CC composition comprising a pharmaceutical carrier and at least one of the
 CC peptide inhibitors cited above, is useful for reducing collagen matrix
 CC turnover in mammals, particularly humans, or for reducing degradation of
 CC one or more collagen proteins. An isolated or purified antibody that
 CC specifically binds to an epitope of the peptide or its antigenic fragment
 CC is used to inhibit the activity of the peptide, to identify inhibitors of
 CC the generation of the peptide, or to identify a subject at risk for rapid
 CC or slow progression of a disease responding to therapy designed to arrest
 CC cartilage degradation or at risk for a disease by showing of early pre-
 CC clinical changes prior to clinical presentation of the disease, where the
 CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
 CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
 CC addition, the antibody is used to detect the release of type II collagen
 CC degradation products in body fluids, e.g. tissue extracts, serum,
 CC synovial fluid or urine. The composition and methods may be used for
 CC diagnosing and treating such diseases. The present sequence represents a
 CC specific example of the peptide effective in altering the rate of
 CC degradation of type II collagen or the rate of chondrocyte hypertrophy.
 XX
 SQ Sequence 24 AA;

Query Match 100.0%; Score 132; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.8e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ERGPPGPGQARGFGTGTGLPGVK 23
 DB 2 ERGPPGPGQARGFGTGTGLPGVK 24

RESULT 3
 ADN12245
 ID ADN12245 standard; peptide; 24 AA.
 XX
 AC ADN12245;

01-JUL-2004 (first entry)

Type II collagen degradation rate altering peptide Pro6.

XX Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
 KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.

XX Synthetic.

Key Location/Qualifiers
 FT Modified-site 15 /note= "hydroxylated proline"
 FT Modified-site 18 /note= "hydroxylated proline"
 FT Modified-site 21 /note= "hydroxylated proline"

XX WO2004031206-A2.

XX 15-APR-2004.

XX 30-SEP-2003; 2003WO-US030744.

XX 30-SEP-2002; 2002US-0414332P.

XX (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.

XX Poole AR;

XX WPI; 2004-316460/29.

XX New peptides that regulate the degradation of type II collagen, useful
 PT for diagnosing and treating for e.g. osteoarthritis, rheumatoid
 PT arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or

PT eye diseases.
XX Claim 1; Page 50; 74pp; English.
PS
XX
XX The invention relates to an isolated or purified peptide comprising a
CC fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III,
CC CB12-IV, Pro6, Pro15, Pro18 or Pro21, or its fragment, conservatively
CC substituted variant, mimetic, inhibitor or homologue. The peptide alters
CC the rate of degradation of type II collagen or the rate of chondrocyte
CC hypertrophy. The peptide or its fragment is hydroxylated at one or more
CC of the proline or lysine residues of the peptide. A pharmaceutical
CC composition comprising a pharmaceutical carrier and at least one of the
CC peptide inhibitors cited above, is useful for reducing collagen matrix
CC turnover in mammals, particularly humans, or for reducing degradation of
CC one or more collagen proteins. An isolated or purified antibody that
CC specifically binds to an epitope of the peptide or its antigenic fragment
CC is used to inhibit the activity of the peptide, to identify inhibitors of
CC the generation of the peptide, or to identify a subject at risk for rapid
CC or slow progression of a disease responding to therapy designed to arrest
CC cartilage degradation or at risk for a disease by showing of early pre-
CC clinical changes prior to clinical presentation of the disease, where the
CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
CC addition, the antibody is used to detect the release of type II collagen
CC degradation products in body fluids, e.g. tissue extracts, serum,
CC synovial fluid or urine. The composition and methods may be used for
CC diagnosing and treating such diseases. The present sequence represents a
CC specific example of the peptide effective in altering the rate of
CC degradation of type II collagen or the rate of chondrocyte hypertrophy.
XX Sequence 24 AA;
SQ

Query Match 100.0%; Score 132; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.8e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFGPTGGLPGVK 23
Db |||||||||||||||||||
2 ERGPPGPGQARGFGPTGGLPGVK 24

RESULT 4
ADN12247
ID ADN12247 standard; peptide; 24 AA.
XX
AC ADN12247;
XX
XX 01-JUL-2004 (first entry)
XX
XX Type II collagen degradation rate altering peptide Pro18.
XX
XX Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 6 /note= "hydroxylated proline"
FT Modified-site 15 /note= "hydroxylated proline"
FT Modified-site 21 /note= "hydroxylated proline"
FT
XX WO2004031206-A2.
PN
XX
XX 15-APR-2004.
XX
XX 30-SEP-2003; 2003WO-US030744.
XX
XX 30-SEP-2002; 2002US-0414332P.
XX
XX (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.

XX Poole AR;
XX WPI; 2004-316460/29.
XX
XX New peptides that regulate the degradation of type II collagen, useful
PT for diagnosing and treating for e.g. osteoarthritis, rheumatoid
PT arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or
PT eye diseases.
XX
XX Claim 1; Page 50; 74pp; English.
XX
XX The invention relates to an isolated or purified peptide comprising a
CC fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III,
CC CB12-IV, Pro6, Pro15, Pro18 or Pro21, or its fragment, conservatively
CC substituted variant, mimetic, inhibitor or homologue. The peptide alters
CC the rate of degradation of type II collagen or the rate of chondrocyte
CC hypertrophy. The peptide or its fragment is hydroxylated at one or more
CC of the proline or lysine residues of the peptide. A pharmaceutical
CC composition comprising a pharmaceutical carrier and at least one of the
CC peptide inhibitors cited above, is useful for reducing collagen matrix
CC turnover in mammals, particularly humans, or for reducing degradation of
CC one or more collagen proteins. An isolated or purified antibody that
CC specifically binds to an epitope of the peptide or its antigenic fragment
CC is used to inhibit the activity of the peptide, to identify inhibitors of
CC the generation of the peptide, or to identify a subject at risk for rapid
CC or slow progression of a disease responding to therapy designed to arrest
CC cartilage degradation or at risk for a disease by showing of early pre-
CC clinical changes prior to clinical presentation of the disease, where the
CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
CC addition, the antibody is used to detect the release of type II collagen
CC degradation products in body fluids, e.g. tissue extracts, serum,
CC synovial fluid or urine. The composition and methods may be used for
CC diagnosing and treating such diseases. The present sequence represents a
CC specific example of the peptide effective in altering the rate of
CC degradation of type II collagen or the rate of chondrocyte hypertrophy.
XX Sequence 24 AA;
SQ

Query Match 100.0%; Score 132; DB 8; Length 24;
Best Local Similarity 100.0%; Pred. No. 8.8e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFGPTGGLPGVK 23
Db |||||||||||||||||||
2 ERGPPGPGQARGFGPTGGLPGVK 24

RESULT 5
ADN12246
ID ADN12246 standard; peptide; 24 AA.
XX
AC ADN12246;
XX
XX 01-JUL-2004 (first entry)
XX
XX Type II collagen degradation rate altering peptide Pro15.
XX
XX Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 6 /note= "hydroxylated proline"
FT Modified-site 18 /note= "hydroxylated proline"
FT Modified-site 21 /note= "hydroxylated proline"
FT
XX WO2004031206-A2.
PN

XX PD 15-APR-2004.
 XX PF 30-SEP-2003; 2003WO-US030744.
 XX PR 30-SEP-2002; 2002US-0414332P.
 XX PA (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
 XX PI Poole AR;
 XX PI WPI; 2004-316460/29.
 XX DR
 XX PT New peptides that regulate the degradation of type II collagen, useful
 XX PT for diagnosing and treating for e.g. osteoarthritis, rheumatoid
 XX PT arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or
 XX PT eye diseases.
 XX PS
 XX PS Claim 1; Page 50; 74pp; English.
 XX CC The invention relates to an isolated or purified peptide comprising a
 XX CC fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III,
 XX CC CB12-IV, Pro6, Pro15, Pro18 or Pro21, or its fragment, conservatively
 XX CC substituted variant, mimetic, inhibitor or homologue. The peptide alters
 XX CC the rate of degradation of type II collagen or the rate of chondrocyte
 XX CC hypertrophy. The peptide or its fragment is hydroxylated at one or more
 XX CC of the proline or lysine residues of the peptide. A pharmaceutical
 XX CC composition comprising a pharmaceutical carrier and at least one of the
 XX CC peptide inhibitors cited above, is useful for reducing collagen matrix
 XX CC turnover in mammals, particularly humans, or for reducing degradation of
 XX CC one or more collagen proteins. An isolated or purified antibody that
 XX CC specifically binds to an epitope of the peptide or its antigenic fragment
 XX CC is used to inhibit the activity of the peptide, to identify inhibitors of
 XX CC the generation of the peptide, or to identify a subject at risk for rapid
 XX CC or slow progression of a disease responding to therapy designed to arrest
 XX CC cartilage degradation or at risk for a disease by showing of early pre-
 XX CC clinical changes prior to clinical presentation of the disease, where the
 XX CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
 XX CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
 XX CC addition, the antibody is used to detect the release of type II collagen
 XX CC degradation products in body fluids, e.g. tissue extracts, serum,
 XX CC synovial fluid or urine. The composition and methods may be used for
 XX CC diagnosing and treating such diseases. The present sequence represents a
 XX CC specific example of the peptide effective in altering the rate of
 XX CC degradation of type II collagen or the rate of chondrocyte hypertrophy.
 XX SQ
 XX SQ Sequence 24 AA;
 Query Match 100.0%; Score 132; DB 8; Length 24;
 Best Local Similarity 100.0%; Pred. No. 8.8e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ERGPPGQARGFGCTPGLPGVK 23
 Db 2 ERGPPGQARGFGCTPGLPGVK 24
 |||||
 RESULT 6
 ADN12240
 ID ADN12240 standard; peptide; 84 AA.
 XX AC
 XX ADN12240;
 XX DT 01-JUL-2004 (first entry)
 XX DE Type II collagen degradation rate altering peptide.
 XX KW Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
 XX KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.
 XX OS Synthetic.
 XX PN WO2004031206-A2.

XX PD 15-APR-2004.
 XX PF 30-SEP-2003; 2003WO-US030744.
 XX PR 30-SEP-2002; 2002US-0414332P.
 XX PA (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
 XX PI Poole AR;
 XX PI WPI; 2004-316460/29.
 XX DR
 XX PT New peptides that regulate the degradation of type II collagen, useful
 XX PT for diagnosing and treating for e.g. osteoarthritis, rheumatoid
 XX PT arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or
 XX PT eye diseases.
 XX PS
 XX PS Disclosure; Page 9; 74pp; English.
 XX CC The invention relates to an isolated or purified peptide comprising a
 XX CC fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III,
 XX CC CB12-IV, Pro6, Pro15, Pro18 or Pro21, or its fragment, conservatively
 XX CC substituted variant, mimetic, inhibitor or homologue. The peptide alters
 XX CC the rate of degradation of type II collagen or the rate of chondrocyte
 XX CC hypertrophy. The peptide or its fragment is hydroxylated at one or more
 XX CC of the proline or lysine residues of the peptide. A pharmaceutical
 XX CC composition comprising a pharmaceutical carrier and at least one of the
 XX CC peptide inhibitors cited above, is useful for reducing collagen matrix
 XX CC turnover in mammals, particularly humans, or for reducing degradation of
 XX CC one or more collagen proteins. An isolated or purified antibody that
 XX CC specifically binds to an epitope of the peptide or its antigenic fragment
 XX CC is used to inhibit the activity of the peptide, to identify inhibitors of
 XX CC the generation of the peptide, or to identify a subject at risk for rapid
 XX CC or slow progression of a disease responding to therapy designed to arrest
 XX CC cartilage degradation or at risk for a disease by showing of early pre-
 XX CC clinical changes prior to clinical presentation of the disease, where the
 XX CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
 XX CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
 XX CC addition, the antibody is used to detect the release of type II collagen
 XX CC degradation products in body fluids, e.g. tissue extracts, serum,
 XX CC synovial fluid or urine. The composition and methods may be used for
 XX CC diagnosing and treating such diseases. The present sequence represents a
 XX CC peptide effective in altering the rate of degradation of type II collagen
 XX CC or the rate of chondrocyte hypertrophy.
 XX SQ
 XX SQ Sequence 84 AA;
 Query Match 100.0%; Score 132; DB 8; Length 84;
 Best Local Similarity 100.0%; Pred. No. 2.7e-08;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ERGPPGQARGFGCTPGLPGVK 23
 Db 25 ERGPPGQARGFGCTPGLPGVK 47
 |||||
 RESULT 7
 ADN12251
 ID ADN12251 standard; peptide; 84 AA.
 XX AC
 XX ADN12251;
 XX DT 01-JUL-2004 (first entry)
 XX DE Type II collagen degradation rate altering peptide.
 XX KW Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
 XX KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.
 XX OS Synthetic.
 XX PN Location/Qualifiers

FT Modified-site 6 /note= "hydroxylated proline"
FT Modified-site 9
FT Modified-site 12 /note= "hydroxylated proline"
FT Modified-site 21 /note= "hydroxylated proline"
FT Modified-site 30 /note= "hydroxylated proline"
FT Modified-site 39 /note= "hydroxylated proline"
FT Modified-site 42 /note= "hydroxylated proline"
FT Modified-site 45 /note= "hydroxylated proline"
FT Modified-site 66 /note= "hydroxylated proline"
FT Modified-site 75 /note= "hydroxylated proline"
FT Modified-site 81 /note= "hydroxylated proline"
FT Modified-site 81 /note= "hydroxylated proline"
XX
XX WO2004031206-A2.
XX
XX 15-APR-2004.
XX
XX 30-SEP-2003; 2003WO-US030744.
XX
XX 30-SEP-2002; 2002US-0414332P.
XX
XX (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
XX-
XX Poole AR;
XX
XX WPI; 2004-316460/29.
XX
XX New peptides that regulate the degradation of type II collagen, useful
PT for diagnosing and treating for e.g. osteoarthritis, rheumatoid
PT arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or
PT eye diseases.
XX
XX Disclosure; Fig 1; 74pp; English.
XX
XX The invention relates to an isolated or purified peptide comprising a
CC fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III,
CC CB12-IV, Pro6, Pro15, Pro18 or Pro21, or its fragment, conservatively
CC substituted variant, mimetic, inhibitor or homologue. The peptide alters
CC the rate of degradation of type II collagen or the rate of chondrocyte
CC hypertrophy. The peptide or its fragment is hydroxylated at one or more
CC of the proline or lysine residues of the peptide. A pharmaceutical
CC composition comprising a pharmaceutical carrier and at least one of the
CC peptide inhibitors cited above, is useful for reducing collagen matrix
CC turnover in mammals, particularly humans, or for reducing degradation of
CC one or more collagen proteins. An isolated or purified antibody that
CC specifically binds to an epitope of the peptide or its antigenic fragment
CC is used to inhibit the activity of the peptide, to identify inhibitors of
CC the generation of the peptide, or to identify a subject at risk for rapid
CC or slow progression of a disease responding to therapy designed to arrest
CC cartilage degradation or at risk for a disease by showing of early pre-
CC clinical changes prior to clinical presentation of the disease, where the
CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
CC addition, the antibody is used to detect the release of type II collagen
CC degradation products in body fluids, e.g. tissue extracts, serum,
CC synovial fluid or urine. The composition and methods may be used for
CC diagnosing and treating such diseases. The present sequence represents a
CC peptide effective in altering the rate of degradation of type II collagen
CC or the rate of chondrocyte hypertrophy.
XX
XX Sequence 84 AA;
SQ

Query Match 100.0%; Score 132; DB 8; Length 84;

Best Local Similarity 100.0%; Pred. No. 2.7e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ERGPPGPGARGPFGTGPLGVK 23
DB 26 ERGPPGPGARGPFGTGPLGVK 48
RESULT 8
ADN12250
ID ADN12250 standard; peptide; 85 AA.
XX AC ADN12250;
XX
XX 01-JUL-2004 (first entry)
XX
XX Type II collagen degradation rate altering peptide CB12.
XX
XX Type II collagen; chondrocyte hypertrophy; osteopathic; antiarthritic;
KW antirheumatic; ophthalmological; gene therapy; cartilage degradation.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Modified-site 6
FT Modified-site /note= "hydroxylated proline"
FT Modified-site 9 /note= "hydroxylated proline"
FT Modified-site 12 /note= "hydroxylated proline"
FT Modified-site 21 /note= "hydroxylated proline"
FT Modified-site 30 /note= "hydroxylated proline"
FT Modified-site 39 /note= "hydroxylated proline"
FT Modified-site 42 /note= "hydroxylated proline"
FT Modified-site 45 /note= "hydroxylated proline"
FT Modified-site 66 /note= "hydroxylated proline"
FT Modified-site 75 /note= "hydroxylated proline"
FT Modified-site 81 /note= "hydroxylated proline"
FT Modified-site 81 /note= "hydroxylated proline"
XX
XX WO2004031206-A2.
XX
XX 15-APR-2004.
XX
XX 30-SEP-2003; 2003WO-US030744.
XX
XX 30-SEP-2002; 2002US-0414332P.
XX
XX (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
XX
XX Poole AR;
XX
XX WPI; 2004-316460/29.
XX
XX New peptides that regulate the degradation of type II collagen, useful
PT for diagnosing and treating for e.g. osteoarthritis, rheumatoid
PT arthritis, post-traumatic osteoarthritis, idiopathic osteoarthritis or
PT eye diseases.
XX
XX Claim 1; Page 50; 74pp; English.
XX
XX The invention relates to an isolated or purified peptide comprising a
CC fully defined amino acid sequence of CB12, CB12-I, CB12-II, CB12-III,
CC CB12-IV, Pro6, Pro15, Pro18 or Pro21, or its fragment, conservatively
CC substituted variant, mimetic, inhibitor or homologue. The peptide alters
CC the rate of degradation of type II collagen or the rate of chondrocyte
CC hypertrophy. The peptide or its fragment is hydroxylated at one or more
CC of the proline or lysine residues of the peptide. A pharmaceutical
CC composition comprising a pharmaceutical carrier and at least one of the
CC peptide inhibitors cited above, is useful for reducing collagen matrix
CC turnover in mammals, particularly humans, or for reducing degradation of
CC one or more collagen proteins. An isolated or purified antibody that
CC specifically binds to an epitope of the peptide or its antigenic fragment
CC is used to inhibit the activity of the peptide, to identify inhibitors of
CC the generation of the peptide, or to identify a subject at risk for rapid
CC or slow progression of a disease responding to therapy designed to arrest
CC cartilage degradation or at risk for a disease by showing of early pre-
CC clinical changes prior to clinical presentation of the disease, where the
CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
CC addition, the antibody is used to detect the release of type II collagen
CC degradation products in body fluids, e.g. tissue extracts, serum,
CC synovial fluid or urine. The composition and methods may be used for
CC diagnosing and treating such diseases. The present sequence represents a
CC peptide effective in altering the rate of degradation of type II collagen
CC or the rate of chondrocyte hypertrophy.

CC hypertrophy. The peptide or its fragment is hydroxylated at one or more
 CC of the proline or lysine residues of the peptide. A pharmaceutical
 CC composition comprising a pharmaceutical carrier and at least one of the
 CC peptide inhibitors cited above, is useful for reducing collagen matrix
 CC turnover in mammals, particularly humans, or for reducing degradation of
 CC one or more collagen proteins. An isolated or purified antibody that
 CC specifically binds to an epitope of the peptide or its antigenic fragment
 CC is used to inhibit the activity of the peptide, to identify inhibitors of
 CC the generation of the peptide, or to identify a subject at risk for rapid
 CC or slow progression of a disease responding to therapy designed to arrest
 CC cartilage degradation or at risk for a disease by showing of early pre-
 CC clinical changes prior to clinical presentation of the disease, where the
 CC disease is selected from osteoarthritis, rheumatoid arthritis, post-
 CC traumatic osteoarthritis, idiopathic osteoarthritis and eye disease. In
 CC addition, the antibody is used to detect the release of type II collagen
 CC degradation products in body fluids, e.g. tissue extracts, serum,
 CC synovial fluid or urine. The composition and methods may be used for
 CC diagnosing and treating such diseases. The present sequence represents a
 CC specific example of the peptide effective in altering the rate of
 CC degradation of type II collagen or the rate of chondrocyte hypertrophy.
 XX
 SQ Sequence 85 AA;

Query Match 100.0%; Score 132; DB 8; Length 85;
 Best Local Similarity 100.0%; Pred. No. 2.7e-08;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFGPTGGLPGVK 23
 Db 26 ERGPPGPGQARGFGPTGGLPGVK 48

RESULT 9
 ADQ18267
 ID ADQ18267 standard; protein; 243 AA.
 AC ADQ18267;

XX 26-AUG-2004 (first entry)
 DT Human soft tissue sarcoma-upregulated protein - SEQ ID 1085.
 DE soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human.
 KW Homo sapiens.
 OS WO2004048938-A2.
 PN 10-JUN-2004.
 XX 26-NOV-2003; 2003WO-US038193.
 PF 26-NOV-2002; 2002US-0429739P.
 PR (PROT-) PROTEIN DESIGN LABS INC.
 PA Aziz N, Ginsburg WM, Zlotnik A;
 PI WPI: 2004-441208/41.
 DR

XX Early detection of soft tissue sarcoma comprises determining expression
 PT of a gene in a first soft tissue sample and a normal soft tissue sample
 PT and comparing the gene expression, also useful in treating soft tissue
 PT sarcoma.

PS Example 2; SEQ ID NO 1085; 210pp; English.

XX The invention relates to a novel method for detecting soft tissue sarcoma
 CC which comprises obtaining a first soft tissue sample from an individual
 CC and a normal soft tissue sample from the same or different individual,
 CC determining the expression of a gene in both samples and comparing the
 CC expression of the gene in both soft tissue samples, where a higher level
 CC of protein expression in the first soft tissue sample indicates the

CC presence of soft tissue sarcoma. The method of the invention has
 CC cytostatic applications and may be useful for detecting soft tissue
 CC sarcoma, possibly via gene therapy or vaccine production. The nucleic
 CC acid sequences may be useful in diagnostic and screening applications.
 CC The current sequence is that of a human soft tissue sarcoma-upregulated
 CC protein of the invention. The current sequence is not shown within the
 CC specification per se but was submitted in CD format by the inventor.
 XX

SQ Sequence 243 AA;

Query Match 100.0%; Score 132; DB 8; Length 243;
 Best Local Similarity 100.0%; Pred. No. 7.1e-08;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFGPTGGLPGVK 23
 Db 167 ERGPPGPGQARGFGPTGGLPGVK 189

RESULT 10
 ADC21544
 ID ADC21544 standard; protein; 1014 AA.

XX AC ADC21544;
 XX DT 18-DEC-2003 (first entry)
 XX DE Human type II collagen protein sequence.

XX triple helix formation sequence; interpolyptide linkage;
 KW rheumatoid arthritis; autoimmune disease; inflammatory disease;
 KW peripheral joint; major histocompatibility complex class II region;
 KW HLA-DR; T cell; joint specific antigen; B cell; type II collagen; CII;
 KW antiarthritic; antirheumatic; immunosuppressive; dermatological;
 KW antiinflammatory; antipsoriatic; antiasthmatic; neuroprotective;
 KW relapsing polycondritis; systemic lupus erythematosus; psoriasis;
 KW asthma; Sjogren's syndrome; multiple sclerosis; human.

XX Homo sapiens.

XX WO2003006603-A2.

XX 23-JAN-2003.

XX 11-JUL-2002; 2002WO-IB004256.

XX 12-JUL-2001; 2001US-0305048P.

XX (AREX-) AREXIS AB.

XX Holmdahl R, Burkhardt H, Engstrom JA, Kihlberg J;

XX WPI: 2003-221724/21.

XX N-PSDB; ADC21545.

XX Composition for treating autoimmune disorders such as rheumatoid
 PT arthritis, comprises three polypeptides, each comprising a triple helix
 PT formation sequence, and at least two interpolyptide linkages.

XX Disclosure; SEQ ID NO 1; 113pp; English.

XX This invention relates to a novel composition comprising three
 CC polypeptides, where each polypeptide comprises a triple helix formation
 CC sequence and at least two interpolyptide linkages such that each
 CC polypeptide is attached to at least one of the other two polypeptides.
 CC Rheumatoid arthritis is an autoimmune, inflammatory disease that affects
 CC peripheral joints. The main genetic association is to the major
 CC histocompatibility complex class II region (HLA-DR), suggesting that T
 CC cell mediated autoimmune recognition of joint specific antigens is
 CC involved in the disease. In addition, B cell mediated autoimmune
 CC responses have been observed in rheumatoid joints. Specifically, B cells
 CC have been detected secreting IGG antibodies specific for type II collagen
 CC (CII). The compounds of the invention may be antiarthritic,

CC antirheumatic, immunosuppressive, dermatological, antiinflammatory,
CC antipsoriatic, antiashmatic or vasoprotective through the enhancement of
CC tolerance to the endogenous polypeptide. The compounds may be useful for
CC diagnosing and treating autoimmune conditions such as rheumatoid
CC arthritis, relapsing polychondritis, systemic lupus erythematosus,
CC psoriasis, chronic stages of aschma, Jorge's syndrome and multiple
CC sclerosis. The present sequence is that of the human type II collagen
CC (CII) protein which was used to identify the peptide epitopes of the
CC invention.

XX Sequence 1014 AA;

Query Match 100.0%; Score 132; DB 7; Length 1014;
Best Local Similarity 100.0%; Pred. No. 2.6e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGARGPPTGGLPGVK 23
Db 65 ERGPPGPGARGPPTGGLPGVK 87

RESULT 11

ABM83560
ID ABM83560 standard; protein; 1417 AA.

XX AC ABM83560;

XX 18-NOV-2004 (first entry)

XX Human diagnostic and therapeutic pproteins SEQ ID NO:3809.

XX gene therapy; human diagnostic and therapeutic polynucleotide; dithp.

XX Homo sapiens.

XX WO2004023973-A2.

XX 25-MAR-2004.

XX 12-SEP-2003; 2003WO-US028227.

XX 12-SEP-2002; 2002US-0410259P.

XX 12-SEP-2002; 2002US-0410260P.

XX (INCY-) INCYTE CORP.

XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
PI Harthorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
PI Xu Y, Kwong M, Pollocky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
PI Patury S, Shi X, Suarez CJ;

XX WPI: 2004-329368/30.

DR N-PSDB; ACN42212.

XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
PT in diagnosing a condition, disease or disorder associated with human
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
PT in gene mapping.

XX Claim 27; Page; 190pp; English.

XX The invention relates to novel diagnostic and therapeutic polynucleotides
CC selected from one of the 2722 sequences defined in the specification. A
CC polynucleotide of the invention may have a use in gene therapy. The human
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
CC used to diagnose a particular condition, disease or disorder associated
CC with human molecules, e.g. cell proliferative disorders,
CC autoimmune/inflammatory disorder, developmental disorder, endocrine
CC disorder, neurological disorders, gastrointestinal disorders, or

CC infections caused by virus, bacteria, fungi or parasite. The dithp
CC molecules may also be used in genetic mapping, in identifying individuals
CC from minute biological samples, in detecting single nucleotide
CC polymorphisms, as molecular weight markers, and for somatic or germline
CC gene therapy. The present sequence represents a dithp protein of the
CC invention. Note: The sequence data for this patent is not represented in
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm

XX Sequence 1417 AA;

Query Match 100.0%; Score 132; DB 8; Length 1417;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGARGPPTGGLPGVK 23

Db 265 ERGPPGPGARGPPTGGLPGVK 287

RESULT 12

AAR59751
ID AAR59751 standard; protein; 1418 AA.

XX AC AAR59751;

XX 25-MAR-2003 (revised)

DT 14-FEB-1995 (first entry)

XX Type II collagen.

XX Collagen; triple helix; articular cartilage; collagenase; degradation;
KW monoclonal antibody; epitope; matrix; metalloproteinase.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..24

FT /label= Signal peptide.

XX WO9414070-A1.

XX 23-JUN-1994.

XX 06-DEC-1993; 93WO-CA000522.

XX 04-DEC-1992; 92US-00984123.

XX (SHRI-) SHRINERS HOSPITALS FOR CRIPPLED CHILDREN.

XX Poole AR, Hollander AP;

XX WPI: 1994-234222/28.

XX Determn. of cartilage degradation - using a monoclonal antibody to
PT measure the amt. of unwound collagen or fragments in samples.

XX Disclosure; Fig 1; 119pp; English.

XX Type II collagen constitutes the bulk of the fibrillar backbone of
CC cartilage matrix. It is composed of a tightly wound triple helix which
CC can only be cleaved by the metalloproteinase collagenase to produce 3/4
CC and 1/4 length alpha chain fragments. The destruction of articular
CC cartilage is due, in part, to the degradation of collagen. Incapable of
CC maintaining its helical structure at physiological temperatures,
CC collagenase-cleaved collagens unwind and become susceptible to further
CC degradation by other proteinases. By producing monoclonal antibodies
CC directed against epitopes which are only revealed when collagen is
CC unwound, the antibodies provide a means of determining the degradation of
CC cartilage in a biological sample. The antibodies do not bind to native
CC helical collagen. Epitopes used in the production of such antibodies are
CC described in AAR59749, AAR59750 and AAR67742. (Updated on 25-MAR-2003 to
CC correct PN field.)

```

XX SQ Sequence 1418 AA;
    Query Match      100.0%; Score 132; DB 2; Length 1418;
    Best Local Similarity 100.0%; Pred. No. 3.5e-07;
    Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFGPTGGLPGVK 23
    |||||
Db 196 ERGPPGPGQARGFGPTGGLPGVK 218

RESULT 13
AAR71703
ID AAR71703 standard; protein; 1418 AA.
XX
AC AAR71703;
XX
DT 25-MAR-2003 (revised)
DT 17-OCT-1995 (first entry)
XX
DE Collagen alpha 1 (II) chain precursor.
XX
KW Collagen; antibody; immunoassay; metabolism; diagnosis; monitoring;
KW disorder; osteoporosis; metastatic progression; Paget's disease;
KW hyperthyroidism; bone; resorption; rheumatoid arthritis; osteoarthritis;
KW vasculitis syndrome.
XX
OS Homo sapiens.
XX
PN WO9508115-A1.
XX
PD 23-MAR-1995.
XX
PF 19-SEP-1994; 94WO-DK000348.
XX
PR 17-SEP-1993; 93DK-00001040.
XX
PA (OSTE-) OSTEOMETER AS.
XX
PI Qvist P, Bonde M;
XX
WPI; 1995-131456/17.
XX
PT Assaying collagen fragments in body fluid by immunoassay - using
PT antibodies raised against synthetic peptide(s) contg. potential
PT crosslinking sites, to diagnose and monitor disorders of collagen
PT metabolism, e.g. osteoporosis.
XX
PS Disclosure (Appendix A); Page 53; 87pp; English.
XX
CC Determination of collagen fragments in body fluids can be achieved by
CC immunoassay using antibodies directed against synthetic peptides derived
CC from collagen which contain sites of potential crosslinking. The method
CC is used to diagnose and monitor treatment of disorders of collagen
CC metabolism (degradation of type I collagen may indicate osteoporosis,
CC metastatic progression, Paget's disease, hyperthyroidism or other
CC conditions involving excessive bone resorption; degradation of type II
CC collagen may indicate rheumatoid arthritis or osteoarthritis; and of type
CC III collagen, vaculitis syndrome). The method can also be used to assess
CC the toxicity of a compound and to test drugs for their effect on collagen
CC metabolism. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 1418 AA;

    Query Match      100.0%; Score 132; DB 2; Length 1418;
    Best Local Similarity 100.0%; Pred. No. 3.5e-07;
    Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFGPTGGLPGVK 23
    |||||
Db 196 ERGPPGPGQARGFGPTGGLPGVK 218

RESULT 14
AAY96124
ID AAY96124 standard; peptide; 1418 AA.
XX
AC AAY96124;
XX
DT 19-DEC-2000 (first entry)
DE Collagen type II alpha-1.
XX
KW Collagen type II; rheumatoid arthritis; osteoarthritis; assay; diagnosis.
XX
OS Homo sapiens.
XX
PN US6110689-A.
XX
PD 29-AUG-2000.
XX
PF 04-NOV-1997; 97US-00963825.
XX
PR 21-JAN-1994; 94US-00187319.
XX
PA (OSTE-) OSTEOMETER AS.
XX
PI Bonde M, Qvist P;
XX
WPI; 2000-586349/55.
XX
PT Assaying type I collagen fragments for diagnosing osteoporosis in
PT postmenopausal woman, involves contacting body fluid with synthetic
PT collagen peptide and antibody and quantifying by competitive binding
PT assay.
XX
PS Disclosure; Col 37-46; 41pp; English.
XX
CC The present sequence is that of human type II collagen alpha-1. The
CC invention is based on the discovery of the presence of particular
CC collagen fragments in body fluids of patients compared with those of
CC healthy subjects. These fragments are generated upon collagen degradation
CC and are partly characterised by the presence of potential sites for
CC crosslinking. A method for assaying collagen fragments in a body fluid
CC sample is based on the competitive binding to immunological binding
CC partners of collagen fragments in the sample and of synthetic peptides
CC derived from collagen and containing crosslinkable sites (see AAY96112-
CC 17). When considering the degradation of type II collagen, the assay can
CC be used as a means of identifying the presence of rheumatoid arthritis
CC and osteoarthritis
XX
SQ Sequence 1418 AA;

    Query Match      100.0%; Score 132; DB 3; Length 1418;
    Best Local Similarity 100.0%; Pred. No. 3.5e-07;
    Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFGPTGGLPGVK 23
    |||||
Db 196 ERGPPGPGQARGFGPTGGLPGVK 218

RESULT 15
AAB35624
ID AAB35624 standard; protein; 1418 AA.
XX
AC AAB35624;
XX
DT 14-FEB-2001 (first entry)
XX
DE Human type II collagen.
XX
KW Type II collagen; arthritis; joint; ds.
XX
OS Homo sapiens.

```


XX US6132976-A.
PN 17-OCT-2000.
XX
XX
XX PD
XX PF 22-JAN-1998; 98US-00010999.
XX PR 04-DEC-1992; 92US-00984123.
XX PR 17-JUL-1995; 95US-00448501.
XX (SHRI-) SHRINERS HOSPITALS FOR CHILDREN.
XX PA
XX PI Billinghamurst RC, Poole AR, Hollander AP;
XX
XX WPI; 2001-006136/01.
XX
XX
PT Detecting cartilage degradation useful for early detection of arthritis
PT or joint damage by contacting the biological sample with an antibody that
PT binds to an epitope of unwound type II collagen chains but not to a
PT native helical collagen.
XX
XX
PS Example 1; Fig 1; 58pp; English.
XX
CC The present invention relates to detecting cartilage degradation in a
CC biological sample by identifying the presence of unwound type II collagen
CC in the sample. The method involves contacting the sample with a
CC monoclonal antibody which only binds an epitope on unwound type II
CC collagen chains. The invention is useful for the early detection of
CC arthritis and joint damage and for monitoring disease related to collagen
XX
SQ Sequence 1418 AA;
Query Match 100.0%; Score 132; DB 4; Length 1418;
Best Local Similarity 100.0%; Pred. No. 3.5e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ERGPPGPGQARGFPPTGLPGVK 23
Db 196 ERGPPGPGQARGFPPTGLPGVK 218
Search completed: October 8, 2005, 00:23:36
Job time : 167 secs

Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2005, 00:06:37 ; Search time 39 Seconds
(without alignments)
56.743 Million cell updates/sec

Title: US-10-674-065-3

Perfect score: 132

Sequence: 1 ERGPPCPQARGFPPTGLPGVK 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries.

Database :

PIR 79:*

1: pirl:*

2: pirl:*

3: pirl:*

4: pirl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	673	1 CGB06C	collagen alpha 1(I
2	132	100.0	1418	2 T45467	collagen alpha 1(I
3	132	100.0	1486	1 B40333	collagen alpha 1(I
4	132	100.0	1487	1 CGHU6C	collagen alpha 1(I
5	132	100.0	1492	2 A40333	collagen alpha 1(I
6	122	92.4	1419	2 A41182	collagen alpha 1(I
7	122	92.4	1487	2 B41182	collagen alpha 1(I
8	118	89.4	402	1 CGB02S	collagen alpha 2(I
9	115	87.1	779	1 CGB01S	collagen alpha 1(I
10	115	87.1	1453	2 S21626	collagen alpha 1(I
11	115	87.1	1454	1 CGHU1S	collagen alpha 1(I
12	112	84.8	140	2 A05249	collagen alpha 1(I
13	112	84.8	671	1 CGRT1S	collagen alpha 1(I
14	112	84.8	1042	1 CGCH1S	collagen alpha 1(I
15	109	82.6	1366	1 CGHU2S	collagen alpha 2(I
16	109	82.6	1373	1 A43291	collagen alpha 2(I
17	103	78.0	964	1 CGCH2S	collagen alpha 2(I
18	94	71.2	1532	2 A61262	collagen alpha 1(X
19	94	71.2	2944	2 A54849	collagen alpha 1(V
20	93	70.5	1689	1 CGM54B	collagen alpha 1(I
21	92	69.7	1690	1 CGHU1B	collagen alpha 4(I
22	92	69.7	1691	1 S22917	collagen alpha 5(I
23	92	69.7	1763	2 S16366	collagen alpha 2(I
24	91	68.9	299	2 T29556	hypothetical prote
25	91	68.9	1668	1 CGHU4B	collagen alpha 1(I
26	90	68.2	518	2 A55840	macrophage bacteri
27	90	68.2	920	2 A45748	collagen alpha 1(V
28	90	68.2	1549	2 I48103	type VII collagen
29	88	66.7	177	2 S37749	collagen alpha 2(X

30	88	66.7	210	2 B44984	collagen - nematod
31	88	66.7	307	2 T19582	hypothetical prote
32	88	66.7	330	2 S46657	collagen alpha 1(X
33	88	66.7	675	2 S20819	collagen alpha 3(I
34	87	65.9	423	2 A41207	collagen 13, nonfi
35	87	65.9	438	2 S53787	collagen alpha cha
36	87	65.9	636	2 S41067	collagen alpha 1(I
37	87	65.9	921	2 S40495	collagen alpha 1(I
38	87	65.9	921	2 S42617	collagen alpha 1(I
39	87	65.9	1464	2 S59856	collagen alpha 1(I
40	87	65.9	1712	1 CGHU2B	collagen alpha 2(I
41	86	65.2	284	2 T28887	collagen dpy-10 -
42	86	65.2	453	2 S18804	collagen alpha 4(I
43	85	64.4	283	2 T29837	hypothetical prote
44	85	64.4	294	2 T29838	hypothetical prote
45	85	64.4	294	2 T29839	hypothetical prote

ALIGNMENTS

RESULT 1

CGB06C

collagen alpha 1(II) chain precursor - bovine (tentative sequence) (fragments)
C;Species: Bos primigenius taurus (cattle)

C;Date: 24-Apr-1984 #sequence revision 17-May-1996 #text change 09-Jul-2004

C;Accession: A90369; A90396; A92210; S03940; A90189; A05039; A02859

R;Miller, E.J.; Lunde, L.G.

Biochemistry 12, 3153-3159, 1973

A;Title: Isolation and characterization of the cyanogen bromide peptides from the alpha
A;Reference number: A90369; MUID:73258693; PMID:4732855

A;Contents: composition of CNBr1 and CNBr4

A;Accession: A90369

A;Molecule type: protein

A;Residues: 1-15 <MFL>

A;Cross-references: UNIPROT:P02459

A;Experimental source: cartilage

A;Note: residues positioned by comparison with human alpha 1(II) chain

R;Butler, W.T.; Miller, E.J.; Finch Jr., J.E.

Biochemistry 15, 3000-3006, 1976

A;Title: The covalent structure of cartilage collagen. Amino acid sequence of the NH-2-
A;Reference number: A90396; MUID:76253504; PMID:782511

A;Contents: fragments CNBr2 (16-18), CNBr3 (19-21), CNBr6 (22-54), CNBr12 (55-138), and

A;Accession: A90396

A;Molecule type: protein

A;Residues: 16-177 <BUT>

A;Experimental source: cartilage

A;Note: order of CNBr peptides determined

R;Butler, W.T.; Finch Jr., J.E.; Miller, E.J.

J. Biol. Chem. 252, 639-643, 1977

A;Title: The covalent structure of cartilage collagen. Evidence for sequence heterogene

A;Reference number: A92210; MUID:77093864; PMID:833147

A;Accession: A92210

A;Molecule type: protein

A;Residues: 139-178, 'Z', 180-184, 'PA', 187-190, 'AS', 193-194, 'T', 196-198 <BU2>

A;Experimental source: cartilage

A;Note: a minor, probably nonallelic, alpha 1(II) component has 143-Ala, 164-Leu, and p

R;Seyer, J.M.; Hasty, K.A.; Kang, A.H.

Eur. J. Biochem. 181, 159-173, 1989

A;Title: Covalent structure of collagen. Amino acid sequence of an arthritogenic cyanog

A;Reference number: S03940; MUID:89231683; PMID:2714276

A;Accession: S03940

A;Molecule type: protein

A;Residues: 139-417 <SEY>

R;Butler, W.T.; Miller, E.J.; Finch Jr., J.E.; Inagami, T.

Biochem. Biophys. Res. Commun. 57, 190-195, 1974

A;Title: Homologous regions of collagen alpha1 (I) and alpha1(II) chains: apparent clus

A;Reference number: A90189; MUID:74163168; PMID:4857180

A;Accession: A90189

A;Molecule type: protein

A;Residues: 418-492 <BU3>

A;Experimental source: cartilage

A;Note: the first 75 residues of CNBr8, which follows CNBr11

A:Residues: 1164-1184,'GPSKGAGNIPGPV',1185-1199 <TIL2>
A:Cross-references: EMBL:M37126; NID:g180808; PIDN:AAA52037.1; PID:g180809
A:Note: mutant sequence from a patient with spondyloepiphyseal dysplasia
R:Chenah, K.S.E.; Stoker, N.G.; Griffin, J.R.; Grosveid, F.G.; Solomon, E.
Proc. Natl. Acad. Sci. U.S.A. 82, 2555-2559, 1985
A:Title: Identification and characterization of the human type II collagen gene (COL2A1)
A:Reference number: A02858; MUID:85190534; PMID:3857598
A:Accession: A02858
A:Molecule type: DNA
A:Residues: 1032-1056,'N',1058-1068,'T',1070-1487 <CHE>
A:Cross-references: GB:J00116; NID:g180395; PIDN:AAA51997.1; PID:g180396
R:Elima, K.; Vuorio, I.; Vuorio, E.
Nucleic Acids Res. 15, 9499-9504, 1987
A:Title: Determination of the single polyadenylation site of the human pro-alpha-1(II)
A:Reference number: A27280; MUID:88067771; PMID:2825137
A:Accession: A27280
A:Molecule type: mRNA
A:Residues: 1175-1487 <ELI>
A:Cross-references: EMBL:X06268; NID:g30096; PIDN:CAA29604.1; PID:g30097
A:Experimental source: fetal epiphyseal cartilage
R:Van der Rest, M.; Rosenberg, L.C.; Olsen, B.R.; Poole, A.R.
Biochem. J. 237, 923-925, 1986
A:Title: Chondrocalcin is identical with the C-propeptide of type II procollagen.
A:Reference number: A57033; MUID:87099927; PMID:3800925
A:Accession: A57033
A:Molecule type: protein
A:Residues: 'XE',1244-1246,'N',1248,'X',1250-1265;1295-1305;1395-1408 <VAN>
A:Note: chondrocalcin identified as released collagen 1(II) chain carboxyl-terminal pro-
R:Strom, C.M.; Upholt, W.B.
Nucleic Acids Res. 12, 1025-1038, 1984
A:Title: Isolation and characterization of genomic clones corresponding to the human ty:
A:Reference number: A21733; MUID:84118798; PMID:6320112
A:Accession: A21733
A:Molecule type: DNA
A:Residues: 1245-1295 <STR1>
A:Cross-references: EMBL:X00339; EMBL:X00298; NID:g394699; PIDN:CAA25092.1; PID:g437897
A:Accession: B21733
A:Molecule type: DNA
A:Residues: 894-909,'PR' <STR2>
A:Cross-references: GB:X01785; NID:g30035; PIDN:CAA25082.1; PID:g1335032
R:Nunez, A.M.; Francomano, C.; Young, M.F.; Martin, G.R.; Yamada, Y.
Biochemistry 24, 6343-6348, 1985
A:Title: Isolation and partial characterization of genomic clones coding for a human pr
gene.
A:Reference number: A24561; MUID:86104139; PMID:3002437
A:Accession: A24561
A:Molecule type: DNA
A:Residues: 1296-1358 <NUN2>
A:Cross-references: GB:M12046; NID:g180017
A:Note: this translation is not annotated in GenBank entry HUMCCT2A, release 111.0
A:Note: the codons given for 1333-Lys (AGG) and 1350-Gly (GCA) are inconsistent with th
R:Sangiorgi, F.O.; Benson-Chanda, V.; de Wet, W.J.; Sobel, M.E.; Tsipouras, P.; Ramirez
Nucleic Acids Res. 13, 2207-2225, 1985
A:Title: Isolation and partial characterization of the entire human pro alpha 1(II) col
A:Reference number: I37249; MUID:85215609; PMID:2987845
A:Accession: S59491
A:Molecule type: DNA
A:Residues: 7-28,'R',99-114;541-578;786-802;1055-1056,'N',1058-1068,'T',1070-1109;1200-
A:Accession: I84453
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 7-28 <SAN2>
A:Cross-references: GB:M23759; NID:g180845; EMBL:X03320; GB:M24938; NID:g30104
A:Note: the GenBank PID is based on an incorrect reading frame
A:Accession: I37250
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 541-560 <SAN3>
A:Cross-references: EMBL:X02378; GB:M23870; NID:g30107; PIDN:CAA26227.1; PID:g929621
A:Accession: I37251

Query Match 100.0%; Score 132; DB 1; Length 1487;
Best Local Similarity 100.0%; Pred. No. 1.7e-08;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ERGPPGPGQARGFGTGTGLPGVK 23
Db	265 ERGPPGPGQARGFGTGTGLPGVK 287
RESULT 5	
A40333	
collagen alpha 1'(II) chain precursor - African clawed frog	
C:Species: Xenopus laevis (African clawed frog)	
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004	
C:Accession: A40333	
R:Su, M.W.; Suzuki, H.R.; Bieker, J.J.; Solursh, M.; Ramirez, F.	
J. Cell Biol. 115, 565-575, 1991	
A:Title: Expression of two nonallelic type II procollagen genes during Xenopus laevis em	
A:Reference number: A40333; MUID:92011898; PMID:1918153	
A:Accession: A40333	
A>Status: nucleic acid sequence not shown	
A:Molecule type: mRNA	
A:Residues: 1-1492 <SUA>	
A:Cross-references: UNIPROT:Q91718; UNIPROT:Q91717; GB:M63596	
A>Note: this sequence is presented as substitution relative to another sequence in a fi	
es they replace; the appropriate interpretation of the sequence figure was reconstructed	
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;	
C:Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix	
F:17-96/Domain: von Willebrand factor type C repeat homology <VWC>	
F:1263-1492/Domain: fibrillar collagen carboxyl-terminal homology <FCC>	
Query Match 100.0%; Score 132; DB 2; Length 1492;	
Best Local Similarity 100.0%; Pred. No. 1.7e-08;	
-Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ERGPPGPGQARGFGTGTGLPGVK 23
Db.	270 ERGPPGPGQARGFGTGTGLPGVK 292
RESULT 6	
A41182	
collagen alpha 1(II) chain precursor - mouse	
C:Species: Mus musculus (house mouse)	
C:Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 13-Aug-1999	
C:Accession: A41182; A44885	
R:Metaeranta, M.; Toman, D.; de Crombrughe, B.; Vuorio, E.	
J. Biol. Chem. 266, 16862-16869, 1991	
A:Title: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and	
A:Reference number: A41182; MUID:91358489; PMID:1885613	
A:Accession: A41182	
A>Status: preliminary; not compared with conceptual translation	
A:Molecule type: DNA	
A:Residues: 1-1419 <MET>	
A:Cross-references: GB:M65161	
R:Cheah, K.S.; Lau, E.T.; Au, P.K.; Tam, P.P.	
Development 111, 945-953, 1991	
A>Note: Expression of the mouse alpha 1(II) collagen gene is not restricted to cartilag	
A:Reference number: A44885; MUID:91347939; PMID:1879363	
A:Accession: A44885	
A:Molecule type: DNA	
A:Residues: 1-28 <CHE>	
A:Cross-references: GB:S63190; NID:G234368; PIDN:AAB:9627.1; PID:G234369	
A>Note: sequence extracted from NCBI backbone (NCBIN:63190, NCBIIP:63192)	
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;	
C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime	
F:1191-1419/Domain: fibrillar collagen carboxyl-terminal homology <FCC>	
Query Match 92.4%; Score 122; DB 2; Length 1419;	
Best Local Similarity 95.7%; Pred. No. 2.7e-07;	
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 ERGPPGPGQARGFGTGTGLPGVK 23
Db	197 ERGLPGPGQARGFGTGTGLPGVK 219

RESULT 7	
B41182	
collagen alpha 1(II) chain precursor (long splice form) - mouse	
C:Species: Mus musculus (house mouse)	
C:Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 09-Jul-2004	
C:Accession: B41182	
R:Metsaeranta, M.; Toman, D.; de Crombrughe, B.; Vuorio, E.	
J. Biol. Chem. 266, 16862-16869, 1991	
A:Title: Mouse type II collagen gene. Complete nucleotide sequence, exon structure, and	
A:Reference number: A41182; MUID:91358489; PMID:1885613	
A:Accession: B41182	
A>Status: preliminary; not compared with conceptual translation	
A:Molecule type: DNA	
A:Residues: 1-1487 <MET>	
A:Cross-references: UNIPROT:Q62031; UNIPROT:Q62032; UNIPROT:Q62033; GB:M65161	
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;	
C:Keywords: alternative splicing; coiled coil; extracellular matrix; glycoprotein; trime	
F:13-91/Domain: von Willebrand factor type C repeat homology <VWC>	
F:1259-1487/Domain: fibrillar collagen carboxyl-terminal homology <FCC>	
Query Match 92.4%; Score 122; DB 2; Length 1487;	
Best Local Similarity 95.7%; Pred. No. 2.8e-07;	
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
QY	1 ERGPPGPGQARGFGTGTGLPGVK 23
Db	265 ERGLPGPGQARGFGTGTGLPGVK 287
RESULT 8	
CG802S	
collagen alpha 2(I) chain - bovine (fragment)	
C:Species: Bos primigenius taurus (cattle)	
C:Date: 12-Aug-1981 #sequence_revision 12-Aug-1981 #text_change 05-Dec-1998	
C:Accession: A90596; A91233; C91224; B91661; A02866	
R:Fietzek, P.P.; Breitkreutz, D.; Kuehn, K.	
Biochim. Biophys. Acta 365, 305-310, 1974	
A:Title: Amino acid sequence of the amino-terminal region of calf skin collagen.	
A:Reference number: A90596; MUID:75036115; PMID:4609475	
A:Accession: A90596	
A:Molecule type: protein	
A:Residues: 1-19 <PIE>	
A:Experimental source: skin	
R:Fietzek, P.P.; Rexrodt, F.W.	
Eur. J. Biochem. 59, 113-118, 1975	
A:Title: The covalent structure of collagen. The amino-acid sequence of alpha2-CB4 from	
A:Reference number: A91233; MUID:76091874; PMID:173531	
A:Accession: A91233	
A:Molecule type: protein	
A:Residues: 16-336 <PI2>	
A:Experimental source: skin	
R:Fietzek, P.P.; Furthmayr, H.; Kuehn, K.	
Eur. J. Biochem. 47, 257-261, 1974	
A:Title: Comparative sequence studies on alpha2-CB2 from calf, human, rabbit and pig-ski	
A:Reference number: A91224; MUID:75008198; PMID:4412529	
A:Accession: C91224	
A:Molecule type: protein	
A:Residues: 337-366 <PI3>	
A:Experimental source: skin	
R:Fietzek, P.P.; Kuehn, K.	
Hoppe-Seyler's Z. Physiol. Chem. 355, 647-650, 1974	
A:Title: The covalent structure of collagen: amino acid sequence of the N-terminal regi	
A:Reference number: A91661; MUID:75059250; PMID:4435743	
A:Accession: B91661	
A:Molecule type: protein	
A:Residues: 367-402 <PI4>	
A:Experimental source: skin	
C:Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are h	
C:Comment: The order of the five CNR peptides in the alpha 2 chain of bovine skin colla	
C:Superfamily: collagen alpha 2(I) chain; fibrillar collagen carboxyl-terminal homology	
C:Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine; hydroxyprol,	

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;5/Modified site: allysine (Lys) #status predicted
F;21,27,36,39,42,54,57,66,72,87,90,93,111,114,120,123,129,138,147,174,177,180,192,207,211
xperimental
F;66,111/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental
F;96,117,132,183/Modified site: 5-hydroxylysine (Lys) #status experimental
F;228,273/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental

Query Match 89.4%; Score 118; DB 1; Length 402;
Best Local Similarity 91.3%; Pred. No. 2.5e-07;
Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ERGPPGPGARGPFGTGLPGVK 23
|||||
Db 74 ERGVPGPGARGPFGTGLPGFK 96
|||||

RESULT 9
CGB01S
collagen alpha 1(I) chain - bovine (tentative sequence) (fragments)
C;Species: Bos primigenius taurus (cattle)
C;Date: 24-Apr-1984 #sequence revision 31-Dec-1993 #text change 09-Jul-2004
C;Accession: A91193; A91229; A91387; A91211; A91201; A91200; A43048; A02853
R;Rautenberg, J.; Timpl, R.; Furchmayr, H.
Eur. J. Biochem. 27, 231-237, 1972

A;Title: Structural characterization of N-terminal antigenic determinants in calf and hu
A;Reference number: A91193; MUID:72255334; PMID:4115172
A;Accession: A91193
A;Molecule type: protein
A;Residues: 1-19 <RAU>
A;Cross-references: UNIPROT:P02453
A;Experimental source: skin
A;Note: The epsilon carbon of Lys-9, by homology with the rat alpha 1(I) chain, is conve
R;Fietzek, P.P.; Kuehn, K.
Eur. J. Biochem. 52, 77-82, 1975

A;Title: The covalent structure of collagen: amino-acid sequence of the cyanogen-bromide
A;Reference number: A91229; MUID:76022320; PMID:1164916
A;Accession: A91229
A;Molecule type: protein
A;Residues: 20-145 <FIE>
A;Experimental source: skin
A;Note: Lys-103 is hydroxylated and binds glucosylgalactose
R;Fietzek, P.P.; Wendt, P.; Kell, I.; Kuehn, K.
FEBS Lett. 26, 74-76, 1972

A;Title: The covalent structure of collagen: amino acid sequence of alpha1-CB3 from calf
A;Reference number: A91387; MUID:73049499; PMID:4673951
A;Accession: A91387
A;Molecule type: protein
A;Residues: 146-294 <F12>
A;Experimental source: skin
R;Fietzek, P.P.; Rexrodt, F.W.; Hopper, K.E.; Kuehn, K.
Eur. J. Biochem. 38, 396-400, 1973

A;Title: The covalent structure of collagen. 2. The amino-acid sequence of alpha1-CB7 fr
A;Reference number: A91211; MUID:74086118; PMID:4359390
A;Accession: A91211
A;Molecule type: protein
A;Residues: 295-562 <F13>
A;Experimental source: skin
R;Wendt, P.; Mark, K.V.D.; Rexrodt, F.; Kuehn, K.
Eur. J. Biochem. 30, 169-183, 1972

A;Title: The covalent structure of collagen. The amino-acid sequence of the 112 residues
A;Reference number: A91201; MUID:73042276; PMID:4343808
A;Accession: A91201
A;Molecule type: protein
A;Residues: 563-675 <WEN>
A;Experimental source: skin
R;Fietzek, P.P.; Rexrodt, F.W.; Wendt, P.; Stark, M.; Kuehn, K.
Eur. J. Biochem. 30, 163-168, 1972

A;Title: The covalent structure of collagen. Amino acid sequence of peptide alpha1-CB6-C
A;Reference number: A91200; MUID:73042275; PMID:4343807
A;Accession: A91200
A;Molecule type: protein
A;Residues: 676-758 <F14>

A;Experimental source: skin
A;Note: Pro-726 is the only 3-hydroxyproline and the only hydroxylated proline in posit
R;Rautenberg, J.; Fietzek, P.; Rexrodt, F.; Becker, U.; Stark, M.; Kuehn, K.
FEBS Lett. 21, 75-79, 1972

A;Title: The amino acid sequence of the carboxyterminal nonhelical cross link region of
A;Reference number: A43048
A;Accession: A43048
A;Molecule type: protein
A;Residues: 759-779 <RA2>
A;Experimental source: skin
C;Comment: Lysines at positions 115, 124, 274, 346, 424, 496, 658, and 670 may be hydro
C;Comment: Prolines in the third position of the tripeptide repeating unit (G-X-Y) are
9, 149, 268, and 217 residues.
C;Comment: The complete chain contains 1052 residues.
C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology
C;Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; trimer;
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 87.1%; Score 115; DB 1; Length 779;
Best Local Similarity 87.0%; Pred. No. 1.1e-06;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ERGPPGPGARGPFGTGLPGVK 23
|||||
Db 81 ERGPPGPGARGPFGTGLPGMK 103
|||||

RESULT 10
S21626
collagen alpha 1(I) chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence revision 25-Apr-1997 #text change 09-Jul-2004
C;Accession: S57243; S16374; A23982; I49559; S39789; I48300; S21626
R;Li, S.W.; Khillan, J.; Prockop, D.J.
Matrix Biol. 14, 593-595, 1994

A;Title: The complete cDNA coding sequence for the mouse pro-alpha-1(I) chain of type I
A;Reference number: S57243
A;Accession: S57243
A;Molecule type: mRNA
A;Residues: 1-1453 <LIS>
A;Cross-references: UNIPROT:P11087; EMBL:U08020; NID:G470673; PIDN:AAA88912.1; PID:G470
R;Metsaeranta, M.; Toman, D.; de Crombrughe, B.; Vuorio, E.
Biochim. Biophys. Acta 1089, 241-243, 1991

A;Title: Specific hybridization probes for mouse type I, II, III and IX collagen mRNAs.
A;Reference number: S16176; MUID:91274355; PMID:2054384
A;Accession: S16374
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1442-1453 <MET>
A;Cross-references: EMBL:X57981; NID:G50484; PIDN:CAA41046.1; PID:G50485
R;French, B.T.; Lee, W.H.; Maul, G.G.
Gene 39, 311-312, 1985

A;Title: Nucleotide sequence of a cDNA clone for mouse proalpha1(I) collagen protein.
A;Reference number: A23982; MUID:86137403; PMID:3841523
A;Accession: A23982
A;Molecule type: mRNA
A;Residues: 518-1128 <PRE>
A;Cross-references: GB:M14423; NID:G192261; PIDN:AAA37333.1; PID:G192262
R;Monson, J.M.; Friedman, J.; McCarthy, B.J.
Mol. Cell. Biol. 2, 1362-1371, 1982

A;Title: DNA sequence analysis of a mouse pro-alpha-1(I) procollagen gene: Evidence for
A;Reference number: I49559; MUID:83141374; PMID:6298597
A;Accession: I49559
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 735-1130 <RES>
A;Cross-references: GB:M17491; NID:G192263; PIDN:AAA37334.1; PID:G192264
R;Harbers, K.; Kuehn, M.; Delius, H.; Jaenisch, R.
Proc. Natl. Acad. Sci. U.S.A. 81, 1504-1508, 1984

A;Title: Insertion of retrovirus into the first intron of alpha1(I) collagen gene leads
A;Reference number: I49557; MUID:84170331; PMID:6324198
A;Accession: I49557

A>Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-25 <RE2>
A:CROSS-references: GB:K01688; NID:gl92246; PIDN:AAA37330.1; PID:g553881
R:Fonton, S.F.; Lamané, S.R.; Hannagan, M.; Stacey, A.; Jaenisch, R.; Bateman, J.P.
Biochim. Biophys. Acta 1216, 469-474, 1993
A>Title: Genomic sequence of mouse COL1A1 encoding the collagen propeptides.
A:Reference number: S39789; MUID:94092741; PMID:8268229
A:Accession: S39789
A:Molecule type: DNA
A:Residues: 1-80, 'E', 82-105, 'D', 107-185, 1031-1201, 'G', 1203-1218, 'E', 1220-1221, 'T', 1223-1
R:Rhodes, K.; Rippe, R.A.; Umezawa, A.; Nehls, M.; Brenner, D.A.; Breindl, M.
Mol. Cell. Biol. 14, 5950-5960, 1994
A>Title: DNA methylation represses the murine alpha 1(I) collagen promoter by an indirect
A:Reference number: I48300; MUID:94344105; PMID:8065328
A:Accession: I48300
A>Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-80, 'E', 82-105, 'D', 107-147 <REF>
A:CROSS-references: EMBL:X54876; NID:g50486; PIDN:CRAA38657.1; PID:g50487
C:Genetics:
A:Gene: COL1A1
A:Introns: 770/3; 788/3; 806/3; 842/3; 860/3; 878/3; 932/3; 968/3; 1004/3; 1022/3; 1058/
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C:Keywords: coiled coil; extracellular matrix; glycoprotein; heterotrimer; triple helix
F:1-22/Domain: signal sequence #status predicted <SIG>
F:33-151/Domain: amino-terminal propeptide #status predicted <PRO>
F:30-89/Domain: von Willebrand factor type C repeat homology <VWC>
F:152-1453/Product: collagen alpha 1(I) chain #status predicted <VAT>
F:1224-1453/Domain: fibrillar collagen carboxyl-terminal homology <FCC>
Query Match 87.1%; Score 115; DB 2; Length 1453;
Best Local Similarity 87.0%; Pred. No. 2e-06;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy* 1 ERGPPGQARGFGTGLPGVK 23
|||||
Db 232 ERGPPGQARGFGTGLPGMK 254
|||||
RESULT 11
CGHUS
collagen alpha 1(I) chain precursor - human
N:Alternate names: procollagen alpha 1(I) chain
C:Species: Homo sapiens (man)
C:Date: 12-Aug-1981 #sequence revision 04-Oct-1996 #text change 09-Jul-2004
C:Accession: I60114; S01143; A93335; I55254; A39943; I55237; A35233; S09400; B90567; S11
5269; A29439; I53466; A02852; I37247
R:D'Alessio, M.; Bernard, M.; Pretorius, P.J.; de Wet, W.; Ramirez, F.; Pretorius, P.J.
Gene 67, 105-115, 1988
A>Title: Complete nucleotide sequence of the region encompassing the first twenty-five e
A:Reference number: I60114; MUID:88329734; PMID:2843432
A:Accession: I60114
A>Status: translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-369, 'L', 371-589 <DAL>
A:CROSS-references: UNIPROT:P02452; UNIPROT:Q14992; UNIPROT:Q16053; UNIPROT:Q13896; UNIB
R:Tromp, G.; Kuivaniemi, H.; Stacey, A.; Shikata, H.; Baldwin, C.T.; Jaenisch, R.; Prock
Biochem. J. 253, 919-922, 1988
A>Title: Structure of a full-length cDNA clone for the prepro-alpha-1(I) chain of human
A:Reference number: S01143; MUID:89025644; PMID:3178743
A:Accession: S01143
A:Molecule type: mRNA
A:Residues: 1-472 <TRO>
A:CROSS-references: EMBL:X07884; NID:g30015; PIDN:CRAA30731.1; PID:g30016; GB:M6546; NID
A>Note: submitted to the EMBL/GenBank/DBJ databases by Prockop, D.J., 13-JUN-1988
R:Chu, M.L.; de Wet, W.; Bernard, M.; Ding, J.F.; Morabito, M.; Myers, J.; Williams, C.;
Nature 310, 337-340, 1984
A>Title: Human proalpha1(I) collagen gene structure reveals evolutionary conservation of
A:Reference number: A93335; MUID:84270697; PMID:6462220
A:Accession: A93335
A:Molecule type: DNA
A:Residues: 1-58, 'Q', 60-181 <CHU>

A:CROSS-references: EMBL:X00820; NID:g35657; PIDN:CNA25394.1; PID:g35658
R:Rossouw, C.M.S.; Vergeer, W.P.; du Plooy, S.J.; Bernard, M.P.; Ramirez, F.; de Wet, W.
J. Biol. Chem. 262, 15151-15157, 1987
A>Title: DNA sequences in the first intron of the human pro-alpha 1(I) collagen gene enh
A:Reference number: 155254; MUID:88033098; PMID:2822714
A:Accession: 155254
A>Status: translation not shown; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-45 <ROS>
A:CROSS-references: GB:J02829; NID:gl80387; PIDN:AAA51993.1; PID:gl80388
R:Bornstein, P.; McKay, J.; Morishima, J.K.; Devarayalu, S.; Gellinas, R.E.
Proc. Natl. Acad. Sci. U.S.A. 84, 8869-8873, 1987
A>Title: Regulatory elements in the first intron contribute to transcriptional control o
A:Reference number: A39943; MUID:88097389; PMID:3480516
A:Accession: A39943
A:Molecule type: DNA
A:Residues: 1-34 <BOR>
A:CROSS-references: GB:J03559; NID:gl80876; PIDN:AAA52052.1; PID:g553238
R:Chu, M.L.; de Wet, W.; Bernard, M.; Ramirez, F.
J. Biol. Chem. 260, 2315-2320, 1985
A>Title: Fine structural analysis of the human pro-alpha 1 (I) collagen gene. Promoter s
A:Reference number: 155237; MUID:85130970; PMID:2857713
A:Accession: 155237
A>Status: translation not shown; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-34 <CH2>
A:CROSS-references: GB:M10627; NID:gl80383; PIDN:AAA51992.1; PID:g553226
R:Wittz, M.K.; Keene, D.R.; Hori, H.; Glanville, R.W.; Steinmann, B.; Rao, V.H.; Hollist
J. Biol. Chem. 265, 6312-6317, 1990
A>Title: In vivo and in vitro noncovalent association of excised alpha1(I) amino-termina
rome, type VII.
A:Reference number: A35233; MUID:90202908; PMID:2318855
A:Accession: A35233
A:Molecule type: protein
A:Residues: 33-52 <WIR>
A>Note: this propeptide fragment remained non-covalently bound to a defective, uncleaved
R:Weil, D.; d'Alessio, M.; Ramirez, F.; de Wet, W.; Cole, W.G.; Chan, D.; Bateman, J.F.
EMBO J. 8, 1705-1710, 1989
A>Title: A base substitution in the exon of a collagen gene causes alternative splicing
A:Reference number: S09400; MUID:89356643; PMID:2767050
A:Accession: S09400
A:Molecule type: mRNA
A:Residues: 156-183 <WEI>
R:Click, E.M.; Bornstein, P.
Biochemistry 9, 4699-4706, 1970
A>Title: Isolation and characterization of the cyanogen bromide peptides from the alpha
A:Reference number: A30567; MUID:71038625; PMID:5529814
A:Contents: CNBR0-1, CNBR2, CNBR4, CNBR5
A:Accession: B90567
A:Molecule type: protein
A:Residues: 162-198, 'Z', 200-201, 'Z', 203-206, 'Z', 208-209, 'Z', 211-228, 'B', 230, 'BB', 233, 'Z',
A:Experimental source: skin
A>Note: evidence for 170-allylsine
R:Baetge, B.; Notbohm, H.; Diebold, J.; Lehmann, H.; Bodo, M.; Deutzmann, R.; Mueller, P.
Eur. J. Biochem. 192, 153-159, 1990
A>Title: A critical crosslink region in human-bone-derived collagen type I. Specific cle
A:Reference number: S11372; MUID:90382436; PMID:2169412
A:Accession: S11372
A:Molecule type: protein
A:Residues: 175-187, 274-287, 'P', 289 <BAE>
A>Note: sequence of collagen alpha 1(S)(I) isolated from bone after pepsin digestion
R:Deak, S.B.; Scholz, P.M.; Amenta, P.S.; Constantinou, C.D.; Levi-Minzi, S.A.; Gonzalez
J. Biol. Chem. 266, 21827-21832, 1991
A>Title: The substitution of arginine for glycine 85 of the alpha 1(I) procollagen chain
operative melting of intact type I collagen.
A:Reference number: I55342; MUID:92042092; PMID:1718984
A:Accession: I55342
A>Status: translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 258-268, 1347-1357 <DEA>
A:CROSS-references: GB:S67495; NID:g239007; PIDN:AAB20350.1; PID:g239008
A>Note: sequences from the 5' and 3' ends only are shown; mutant sequence 263-Arg report
R:Morgan, P.H.; Jacobs, H.G.; Segrest, J.P.; Cunningham, L.W.

J. Biol. Chem. 245, 5042-5048, 1970
 A;Title: Comparative study of glycopeptides derived from selected vertebrate collagens.
 A;Reference number: A92069; MUID:71001508; PMID:4319110
 A;Accession: A92069
 A;Molecule type: protein
 A;Residues: 263-268 <MOR>
 A;Experimental source: skin
 A;Note: Attachment of 2-O-alpha-D-glucosyl-O-beta-D-galactose to 5-hydroxylysine
 R;Labhard, M.E.; Hollister, D.W.
 Matrix 10, 124-130, 1990
 A;Title: Segmental amplification of the entire helical and telopeptide regions of the ch
 A;Reference number: S15989; MUID:90326017; PMID:2374517
 A;Accession: S15989
 A;Molecule type: mRNA
 A;Residues: 281-302;402-420;823-843;925-944;1026-1045;1143-1162 <LAB>
 R;Wirtz, M.K.; Rao, V.H.; Glanville, R.W.; Labhard, M.E.; Pretorius, P.J.; de Vries, W.N
 Connect. Tissue Res. 29, 1-11, 1993
 A;Title: A cysteine for glycine substitution at position 175 in an alpha 1 (I) chain of
 A;Reference number: I52905; MUID:93339042; PMID:8339541
 A;Accession: I52905
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 342-352, 'C', 354-359 <W2>
 A;Cross-references: GB:S64717; NID:G408195; PIDN:AAB27677.1; PID:G408196
 A;Note: Mutant sequence from patient with osteogenesis imperfecta
 R;Bernard, M.P.; Chu, M.L.; Myers, J.C.; Ramirez, F.; Eikenberry, E.F.; Prockop, D.J.
 Biochemistry 22, 5213-5223, 1983
 A;Title: Nucleotide sequences of complementary deoxyribonucleic acids for the proalpha
 A;Reference number: A90476; MUID:84080385; PMID:6689127
 A;Accession: A90476
 A;Molecule type: DNA
 A;Residues: 425-1250, 'X', 1252-1328, 'S', 1330-1390, 'X', 1392-1464 <BER>
 A;Cross-references: GB:K01228; NID:G180391; PIDN:AAAS1995.1; PID:G180392
 A;Note: sequence partially completed for missing nucleotides by A29439
 R;Chu, M.L.; Gargiulo, V.; Williams, C.J.; Ramirez, F.
 J. Biol. Chem. 260, 691-694, 1985
 A;Title: Multixon deletion in an osteogenesis imperfecta variant with increased type II
 A;Reference number: A22161; MUID:85104934; PMID:2981843
 A;Accession: A22161
 A;Molecule type: DNA
 A;Residues: 472-594, 'R', 596-607 <CH3>
 A;Cross-references: GB:K03178; GB:K03179; NID:G179612; NID:G179613; PIDN:AAAS1847.1; PID
 A;Note: the authors translated the codon CGT for residue 595 as Pro
 R;Wallis, G.A.; Starman, B.J.; Zinn, A.B.; Byers, P.H.
 Am. J. Hum. Genet. 46, 1034-1040, 1990
 A;Title: Variable expression of osteogenesis imperfecta in a nuclear family is explained
 A;Reference number: A35336; MUID:90252792; PMID:2339700
 A;Accession: A35336
 A;Molecule type: mRNA
 A;Residues: 710-720, 'E', 722-737, 'E', 739-745 <WAL>
 A;Note: the authors translated the codons CAG for 721 and CGT for 738 as Glu
 R;Forlino, A.; Zolerzi, F.; Valli, M.; Pignatti, P.F.; Cetta, G.; Brunelli, P.C.; Motte
 Hum. Mol. Genet. 3, 2201-2206, 1994
 A;Title: Severe (type III) osteogenesis imperfecta due to glycine substitutions in the c
 A;Reference number: I54365; MUID:95187161; PMID:7881420
 A;Accession: I54365
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 746-766, 'S', 768-781 <FOR>
 A;Cross-references: GB:L47667; NID:G1009093; PIDN:AAB59576.1; PID:G1009094
 R;Chessler, S.D.; Wallis, G.A.; Byers, P.H.
 J. Biol. Chem. 268, 18218-18225, 1993
 A;Title: Mutations in the carboxyl-terminal propeptide of the pro alpha 1(I) chain of ty
 A;Reference number: A47426; MUID:93352646; PMID:8349697
 A;Accession: A47426
 A;Molecule type: mRNA
 A;Residues: 1179-1276, 'H', 1278-1336, 1339-1387, 'R', 1389-1464 <CHE>
 A;Cross-references: GB:S64596; NID:G407589; PIDN:AAB27856.1; PID:G407590
 A;Note: sequence extracted from NCBI backbone (NCBIN:136444, NCBI:P136445)
 A;Note: does not represent an experimentally determined sequence but three different mut
 A;Accession: B47426
 A;Molecule type: mRNA

A;Residues: 1179-1464 <CH4>
 A;Experimental source: normal dermal fibroblast culture
 A;Accession: C47426
 A;Molecule type: mRNA
 A;Residues: 1179-1276, 'H', 1278-1464 <CH5>
 A;Experimental source: fetal cell 86-237
 A;Accession: D47426
 A;Molecule type: mRNA
 A;Residues: 1179-1336, 1339-1464 <CH6>
 A;Experimental source: fetal cell 86-146
 A;Accession: E47426
 A;Molecule type: mRNA
 A;Residues: 1179-1387, 'R', 1389-1464 <CH7>
 A;Experimental source: fetal cell 88-251
 R;Cohn, D.H.; Apone, S.; Eyre, D.R.; Starman, B.J.; Andreassen, P.; Charbonneau, H.; N
 J. Biol. Chem. 263, 14605-14607, 1988
 A;Title: Substitution of Cysteine for Glycine within the Carboxyl-terminal Telopeptide
 A;Reference number: I55269; MUID:89008319; PMID:3170557
 A;Accession: I55269
 A;Status: translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1187-1194, 'C', 1196-1220 <COH>
 A;Cross-references: GB:M23213; NID:G340842; PIDN:AAB59363.1; PID:G499622
 A;Note: Mutant sequence from a patient with mild osteogenesis imperfecta
 R;Maekelae, J.K.; Raassina, M.; Virta, A.; Vuorio, E.
 Nucleic Acids Res. 16, 349, 1988
 A;Title: Human pro-alpha-1(I) collagen: cDNA sequence for the C-propeptide domain.
 Query Match 87.1%; Score 115; DB 1; Length 1464;
 Best Local Similarity 87.0%; Pred. No. 2e-06;
 Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ERGPPGPGQARGFPPTGPGVGVK 23
 |||||:|||||:|||||:|||||:
 Db 243 ERGPPGPGQARGLPGTAGLPGMK 265
 |||||:|||||:|||||:|||||:
 RESULT 12
 A05249
 collagen alpha 1(I) chain precursor - baboon (tentative sequence) (fragment)
 C;Species: Papio sp. (baboon)
 C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004
 C;Accession: A05249
 R;Epstein Jr., E.H.; Scott, R.D.; Miller, E.J.; Piez, K.A.
 J. Biol. Chem. 246, 1718-1724, 1971
 A;Title: Isolation and characterization of the peptides derived from soluble human and
 A;Reference number: A92078; MUID:71134791; PMID:4993958
 A;Contents: CNBr0-1, CNBr2, CNBr4, CNBr5, composition
 A;Accession: A05249
 A;Molecule type: protein
 A;Residues: 1-140 <EPS>
 A;Cross-references: UNIPROT:Q7M2Y1
 A;Experimental source: skin
 C;Comment: Prolines at the third position of the tripeptide repeating unit (G-X-Y) are i
 C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology
 C;Keywords: coiled coil; extracellular matrix; glycoprotein; skin; trimer; triple helix
 Query Match 84.8%; Score 112; DB 2; Length 140;
 Best Local Similarity 78.3%; Pred. No. 5.1e-07;
 Matches 18; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ERGPPGPGQARGFPPTGPGVGVK 23
 |||||:|||||:|||||:|||||:
 Db 82 ZRGPPGPGARGLPGTAGLPGMK 104
 |||||:|||||:|||||:|||||:
 RESULT 13
 CGRT15
 collagen alpha 1(I) chain - rat (tentative sequence) (fragments)
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 31-Mar-2000
 C;Accession: A90559; A90552; A92029; A90362; A90566; A90362; A90379; A91209; A9
 R;Bornstein, P.

Biochemistry 8, 63-71, 1969
A:Title: Comparative sequence studies of rat skin and tendon collagen. II. The absence of
A:Reference number: A90559; MUID:69155173; PMID:5777344
A:Contents: CNB+0 and CNB+1
A:Accession: A90559
A:Molecule type: protein
A:Residues: 1-19 <BOL>
A:Experimental source: tendon
A:Note: sequences from skin and tendon appear to be identical
A:Note: the amino-terminal tetrapeptide may be removed by limited proteolysis during ext
R:Kang, A.H.; Bornstein, P.; Piez, K.A.
Biochemistry 6, 788-795, 1967
A:Title: The amino acid sequence of peptides from the cross-linking region of rat skin c
A:Reference number: A90552; MUID:67162268; PMID:5337886
A:Contents: CNB+1
A:Accession: A90552
A:Molecule type: protein
A:Residues: 5-19 <KAN>
A:Experimental source: skin
R:Bornstein, P.
J. Biol. Chem. 242, 2572-2574, 1967
A:Title: The incomplete hydroxylation of individual prolyl residues in collagen.
A:Reference number: A92029; MUID:67165368; PMID:4290711
A:Contents: CNB+2
A:Accession: A92029
A:Molecule type: protein
A:Residues: 20-55 <BO2>
A:Experimental source: skin and tendon
R:Butler, W.T.; Ponder, S.L.
Biochemistry 10, 2076-2081, 1971
A:Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino a
A:Reference number: A90353; MUID:71263178; PMID:4327399
A:Contents: CNB+4
A:Accession: A90353
A:Molecule type: protein
A:Residues: 56-102 <BU1>
A:Experimental source: skin
R:Butler, W.T.
Biochemistry 9, 44-50, 1970
A:Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. The cov
A:Reference number: A90566; MUID:70085124; PMID:5411206
A:Contents: CNB+5
A:Accession: A90566
A:Molecule type: protein
A:Residues: 103-139 <BU2>
A:Experimental source: skin
R:Ballan, G.; Click, E.M.; Bornstein, P.
Biochemistry 10, 4470-4478, 1971
A:Title: Structure of rat skin collagen alphas 1(I)-C88. Amino acid sequence of the hydroxyla
A:Reference number: A90357; MUID:72136131; PMID:4335087
A:Contents: CNB+8
A:Accession: A90357
A:Molecule type: protein
A:Residues: 140-238 <BA1>
A:Experimental source: skin
R:Ballan, G.; Click, E.M.; Hermodson, M.A.; Bornstein, P.
Biochemistry 11, 3798-3806, 1972
A:Title: Structure of rat skin collagen alphas 1(I)-C88. Amino acid sequence of the hydroxyla
A:Reference number: A90362; MUID:73006942; PMID:4342027
A:Contents: CNB+8
A:Accession: A90362
A:Molecule type: protein
A:Residues: 239-418 <BA2>
A:Experimental source: skin
R:Butler, W.T.; Underwood, S.P.; Finch Jr., J.E.
Biochemistry 13, 2946-2953, 1974
A:Title: Chemical studies on the cyanogen bromide peptides of rat skin collagen. Amino a
A:Reference number: A90379; MUID:74271984; PMID:4366532
A:Contents: CNB+3
A:Accession: A90379
A:Molecule type: protein
A:Residues: 419-567 <BU3>
A:Experimental source: skin

R:Stoltz, M.; Timpl, R.; Furthmayr, H.; Kuehn, K.
Eur. J. Biochem. 37, 287-294, 1973
A:Title: Structural and immunogenic properties of a major antigenic determinant in neur
A:Reference number: A91209; MUID:74011954; PMID:4126850
A:Contents: CNB+6
A:Accession: A91209
A:Molecule type: protein
A:Residues: 568-651 <ST1>
A:Experimental source: skin
A:Note: this region probably corresponds to positions 949-1032 of the alpha 1(I) chain
A:Note: the major antigenic determinant (of neutral salt-extracted rat skin collagen) in
R:Stoltz, M.; Timpl, R.; Kuehn, K.
FEBS Lett. 26, 61-65, 1972
A:Title: Non-helical regions in rat collagen alpha-chain.
A:Reference number: A91385; MUID:73049495; PMID:4636751
A:Contents: CNB+6
A:Accession: A91385
A:Molecule type: protein
A:Residues: 651-671 <ST2>
A:Experimental source: skin
A:Note: the composition of peptides comprising residues 1-9 and 1-19 confirms the sequen
A:Note: this region (residues 651-671 above) probably corresponds to positions 1032-1052
C:Comment: Prolines and lysines at the third position of the tripeptide repeating unit
ed and subsequently O-glycosylated.
C:Comment: The order of the nine CNBr peptides in the alpha 1(I) chain of rat skin colla
C:Comment: The complete chain contains 1052 residues.
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C:Keywords: blocked amino end; coiled coil; extracellular matrix; glycoprotein; hydroxyl
F:1/Modified site: blocked amino end (Glx) (probably pyrrolidone carboxylic acid) #statu
F:9/Modified site: allysine (Lys) #status experimental
F:103,424,547/Binding site: carboxylate (Lys) (covalent) #status experimental
F:103/Modified site: 5-hydroxylysine (Lys) #status experimental
F:424,547/Modified site: 5-hydroxylysine (Lys) (partial) #status experimental
Query Match 84.8%; Score 112; DB 1; Length 671;
Best Local Similarity 82.6%; Pred. No. 2,2e-06;
Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 1 ERGPPGPGARGFPPTGGLPGVK 23
:|||||:|||||:|||||:
Db 81 QRGPFGPGARGLPGTGLPGMK 103
RESULT 14
CCHLS
collagen alpha 1(I) chain - chicken (tentative sequence) (fragments)
C:Species: Gallus gallus (chicken)
C:Date: 12-Aug-1981 #sequence revision 06-Jul-1982 #text_change 31-Mar-2000
C:Accession: A90458; A90181; A92857
R:Highberger, J.H.; Corbett, C.; Dixit, S.N.; Yu, W.; Seyer, J.M.; Kang, A.H.; Gross, J
Biochemistry 21, 2048-2055, 1982
A:Title: Amino acid sequence of chick skin collagen alpha 1(I)-C88 and the complete prim
A:Reference number: A90458; MUID:82231995; PMID:7093229
A:Accession: A90458
A:Molecule type: protein
A:Residues: 1-1036 <HIC>
A:Experimental source: skin
A:Note: this is the latest in a series of papers from these workers elucidating the seq
R:Eyre, D.R.; Glimcher, M.J.
Biochem. Biophys. Res. Commun. 48, 720-726, 1972
A:Title: Evidence for a previously undetected sequence at the carboxyterminus of the al
A:Reference number: A90181; MUID:72243016; PMID:5047697
A:Accession: A90181
A:Molecule type: protein
A:Residues: 1037-1042 <EYR>
A:Experimental source: skin
A:Note: residues 1037-1042 above correspond to the carboxyl end of the protein
C:Comment: Lysines at positions 103, 700, 934, and 946 above may be hydroxylated in som
C:Comment: Most of the prolines at the third position of the tripeptide repeating unit
C:Comment: Pro-1002 is the only 3-hydroxyproline and the only hydroxylated proline in p
C:Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;
C:Keywords: coiled coil; extracellular matrix; glycoprotein; pyroglutamic acid; trimer;
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental


```

Query Match      82.6%;   Score 109;   DB 1;   Length 1366;
Best Local Similarity 87.0%;   Pred. No. 1e-05;
Matches 20;   Conservative 0;   Mismatches 3;   Indels 0;   Gaps 0;

Qy      1  ERGPPPGQARGPFGTGLPGVK 23
      |||  |||  |||  |||  |||  |||  |||
Db      155  ERGVVPGQARGPFGTGLPGFK 177

Search completed: October 8, 2005, 00:27:22
Job time : 39 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2005, 00:04:32 ; Search time 176 Seconds
(without alignments)
66.919 Million cell updates/sec

Title: US-10-674-065-3

Perfect score: 132
Sequence: 1 ERGPPPGQARGFGPTGLPGVK 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03.*

1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	132	100.0	243	Q14045	Q14045 homo sapien
2	132	100.0	747	1 CA12 BOVIN	P02459 bos taurus
3	132	100.0	1160	2 Q14046	Q14046 homo sapien
4	132	100.0	1269	2 Q7T227	Q7T227 gallus gall
5	132	100.0	1418	1 CA12 HUMAN	Q28458 homo sapien
6	132	100.0	1418	2 Q28396	Q28396 equus caball
7	132	100.0	1418	2 Q9W7R9	Q9W7R9 cynops pyrr
8	132	100.0	1420	2 Q90W37	Q90W37 gallus gall
9	132	100.0	1486	2 Q91717	Q91717 xenopus lae
10	132	100.0	1486	2 Q7ZTI6	Q7ZTI6 xenopus lae
11	132	100.0	1487	2 Q14047	Q14047 homo sapien
12	132	100.0	1487	2 Q77753	Q77753 canis famil
13	132	100.0	1491	2 Q91718	Q91718 xenopus lae
14	132	100.0	1491	2 Q7ZTM4	Q7ZTM4 xenopus lae
15	132	100.0	1492	2 Q6P4Z2	Q6P4Z2 xenopus tro
16	131	99.2	1447	2 Q6P4U1	Q6P4U1 brachydanio
17	131	99.2	1447	2 Q6U1J5	Q6U1J5 brachydanio
18	132	92.4	1419	2 Q63123	Q63123 rattus norv
19	132	92.4	1419	2 Q80VY3	Q80VY3 mus musculu
20	132	92.4	1419	2 Q80X38	Q80X38 mus musculu
21	132	92.4	1487	2 Q641K3	Q641K3 mus musculu
22	118	89.4	1355	1 CA12 RANCA	Q42350 rana catesb
23	117	88.6	1442	2 Q62031	Q62031 mus musculu
24	117	88.6	1442	2 Q62033	Q62033 mus musculu
25	117	88.6	1459	1 CA12 MOUSE	P28481 mus musculu
26	117	88.6	1459	2 Q62032	Q62032 mus musculu
27	115	87.1	187	2 Q9BDZ2	Q9BDZ2 macaca mul
28	115	87.1	343	2 Q46388	Q46388 equus caball
29	115	87.1	779	1 CA11 BOVIN	P02453 bos taurus
30	115	87.1	1069	2 Q6LAN8	Q6LAN8 homo sapien
31	115	87.1	1225	2 Q6PCL3	Q6PCL3 mus musculu

RESULT 1

Q14045 PRELIMINARY; PRT; 243 AA.
AC Q14045;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-JAN-1999 (Tremblrel. 09, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Collagen II alpha 1 chain (Fragment).
GN Name=COL2A1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human fetal sternum;
RX MEDLINE=91153296; PubMed=1999183;
RA Huang M.C., Seyer J.M., Thompson J.P., Spinella D.G., Cheah K.S.,
RA Kang A.H.;
RT "Genomic organization of the human procollagen alpha 1(II) collagen
RT gene.";
RL Eur. J. Biochem. 195:593-600(1991).
DR EMBL; X57010; CAA40330.1; -.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro: IPR008161; Clg_helix.
DR InterPro: IPR008160; Collagen.
DR Pfam: PF01391; Collagen; 4.
DR ProDom: PD000007; Clg_helix; 1.
FT NON_TER
SQ SEQUENCE 243 AA; 22697 MW; 021130E04652F69B CRC64;
Query Match 100.0%; Score 132; DB 2; Length 243;
Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPPGQARGFGPTGLPGVK 23

DB 167 ERGPPPGQARGFGPTGLPGVK 189

RESULT 2

CA12_BOVIN STANDARD; PRT; 747 AA.
ID CA12_BOVIN
AC P02459; Q28070; Q9XT24;
DT 21-JUL-1986 (Rel. 01, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Collagen alpha 1(II) chain precursor (Fragments).
GN Name=COL2A1;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC

```

OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1] SEQUENCE OF 1-15.
RP TISSUE=Cartilage;
RC MEDLINE=73258693; PubMed=4732855;
RX Miller E.J., Lunde L.G.;
RA "Isolation and characterization of the cyanogen bromide peptides from
RT the alpha 1(II) chain of bovine and human cartilage collagen.";
RL Biochemistry 12:3153-3159(1973).
RN [2] SEQUENCE OF 16-177.
RP TISSUE=Cartilage;
RC MEDLINE=76253504; PubMed=782511;
RX Butler W.T., Miller E.J., Finch J.E. Jr.;
RA "The covalent structure of cartilage collagen. Amino acid sequence of
RT the NH2-terminal helical portion of the alpha 1 (II) chain.";
RL Biochemistry 15:3000-3006(1976).
RN [3] SEQUENCE OF 139-198.
RP TISSUE=Cartilage;
RC MEDLINE=77093864; PubMed=833147;
RX Butler W.T., Finch J.E. Jr., Miller E.J.;
RA "The covalent structure of cartilage collagen. Evidence for sequence
RT heterogeneity of bovine alpha1(II) chains.";
RL J. Biol. Chem. 252:639-643(1977).
RN [4] SEQUENCE OF 139-417.
RP TISSUE=Cartilage;
RC MEDLINE=89231683; PubMed=2714276;
RX Seyer J.M., Haasty K.A., Kang A.H.;
RA "Covalent structure of collagen. Amino acid sequence of an
RT arthrogenic cyanogen bromide peptide from type II collagen of bovine
RL cartilage.";
RN [5] Eur. J. Biochem. 181:159-173(1989).
RN [6] SEQUENCE OF 418-492, HYDROXYLATION SITES LYS-9; LYS-102; LYS-114;
RP LYS-123; LYS-189; LYS-423 AND LYS-435, AND CARBOHYDRATE-LINKAGE SITES
RT LYS-9; LYS-102; LYS-114; LYS-123; LYS-189; LYS-423 AND LYS-435.
RX MEDLINE=74163168; PubMed=4857180;
RA Butler W.T., Miller E.J., Finch J.E. Jr., Inagami T.;
RT "Homologous regions of collagen alpha1(II) and alpha1(I) chains:
RL apparent clustering of variable and invariant amino acid residues.";
RN Biochem. Biophys. Res. Commun. 57:190-195(1974).
RN [7] SEQUENCE OF 180-272 FROM N.A.
RP TISSUE=Cartilage;
RC MEDLINE=94194070; PubMed=7511638;
RX Brand D.D., Myers L.K., Terato K., Whittington K.B., Stuart J.M.,
RA Rosloniec E.F.;
RT "Characterization of the T cell determinants in the induction of
RL autoimmune arthritis by bovine alpha 1(II)-CB11 in H-2q mice.";
RN J. Immunol. 152:3088-3097(1994).
RN [8] SEQUENCE OF 417-566 FROM N.A.
RP TISSUE=Cartilage;
RC MEDLINE=99410731; PubMed=10479530; DOI=10.1006/clim.1999.4755;
RX Tang B., Chiang T.M., Brand D.D., Gumanovskaya M.L., Stuart J.M.,
RA Kang A.H., Myers L.K.;
RT "Molecular definition and characterization of recombinant bovine CB8
RL and CB10: immunogenicity and arthritogenicity.";
RN Clin. Immunol. 92:256-264(1999).
RN [9] SEQUENCE OF 567-747 FROM N.A.
RP MEDLINE=85215651; PubMed=2582365;
RX Sangiorgi F.O., Benson-Chanda V., de Wet W.J., Sobel M.E., Ramirez F.;
RT "Analysis of cDNA and genomic clones coding for the pro alpha 1 chain
RL of calf type II collagen.";
CC CC -!- FUNCTION: Collagen type II is specific for cartilaginous tissues.
CC It is essential for the normal embryonic development of the
CC skeleton, for linear growth and for the ability of cartilage to
CC resist compressive forces.

```

```

CC CC -!- SUBUNIT: Homotrimers of alpha 1(II) chains.
CC CC -!- PTM: Proline residues at the third position of the tripeptide
CC repeating unit (G-X-Y) are hydroxylated in some or all of the
CC chains. Hydroxylation on Pro-9 is involved in cross-linking.
CC CC -!- PTM: O-linked glycans consist of Glc-Gal disaccharides bound to
CC the oxygen atom of post-translationally added hydroxyl groups.
CC CC -!- SIMILARITY: Belongs to the fibrillar collagen family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L28918; AAA30436.1; -.
CC DR EMBL; AF138957; AAD42347.1; -.
CC DR EMBL; X02420; CAA26269.1; -.
CC DR PIR; A90369; GGB06C.
CC DR PIR; I45876; I45876.
CC DR InterPro; IPR008161; Clg_helix.
CC DR InterPro; IPR008160; Collagen.
CC DR InterPro; IPR00885; Fib_collagen_C.
CC DR InterPro; IPR001007; VWFC.
CC DR ProDom; PD000007; Clg_helix; 3.
CC DR ProDom; PD002078; Fib_collagen_C; 1.
CC DR PROSITE; PS01208; VWFC_1; PARTIAL.
CC KW Collagen; Direct protein sequencing; Extracellular matrix;
CC Glycoprotein; Hydroxylation; Repeat; Structural protein.
CC FT CHAIN 1 >566
CC FT NON_CONS 566 567
CC FT PROPEP <567 747
CC FT MOD_RES 9 9
CC FT MOD_RES 102 102
CC FT MOD_RES 114 114
CC FT MOD_RES 123 123
CC FT MOD_RES 189 189
CC FT MOD_RES 423 423
CC FT MOD_RES 435 435
CC FT CARBOHYD 9
CC FT CARBOHYD 102
CC FT CARBOHYD 114
CC FT CARBOHYD 123
CC FT CARBOHYD 189
CC FT CARBOHYD 423
CC FT CARBOHYD 435
CC FT CARBOHYD 648
CC FT VARIANT 143 143
CC FT VARIANT 164 164
CC FT CONFLICT 179 179
CC FT CONFLICT 185 186
CC FT CONFLICT 191 192
CC FT CONFLICT 195 195
CC FT CONFLICT 215 215
CC FT CONFLICT 227 227
CC FT CONFLICT 251 251
CC FT CONFLICT 258 258
CC FT CONFLICT 261 261
CC FT CONFLICT 492 492
CC FT CONFLICT 747 747
CC SQ SEQUENCE 747 AA; 71329 MW; D0FC1D7CD1CA77C CRC64;
CC
CC Query Match 100.0%; Score 132; DB 1; Length 747;
CC Best Local Similarity 100.0%; Pred. NO. 2.1e-07;
CC Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 ERGPPGPGQARGFRGTPTGLPGVK 23
CC |||||
CC DB 80 ERGPPGPGQARGFRGTPTGLPGVK 102
CC
CC RESULT 3
CC Q14046

```

ID Q14046 PRELIMINARY; PRT; 1160 AA.
AC Q14046;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE COL2A1 protein precursor (Fragment).
GN Name=COL2A1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RX MEDLINE=90026318; PubMed=2803268;
RA Baldwin C.T., Reginato A.M., Smith C., Jimenez S.A., Prockop D.J.;
RT "Structure of cDNA clones coding for human type II procollagen. The
RT alpha 1(II) chain is more similar to the alpha 1(I) chain than two
RT other alpha chains of fibrillar collagens.";
RL Biochem. J. 262:521-528(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Cartilage;
RA Prockop D., Baldwin C.T., Reginato A.M., Smith C., Jimenez S.;
RL Submitted (NOV-1989) to the EMBL/GenBank/DBJ databases.
DR EMBL; X16711; CAA34683.1; -;
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR GO; GO:0008817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg helix.
DR InterPro; IPR008160; Collagen.
DR Pfam; PF01391; Collagen; 18.
DR- Probom; PD000007; Clg helix; 6.
KW Collagen; Matrix protein; Signal.
FT SIGNAL 1 23 Potential.
FT CHAIN 113 >1160 collagen.
FT NON_TER 1160 1160
SQ SEQUENCE 1160 AA; 105630 MW; A7F0523B856C8639 CRC64;

Query Match 100.0%; Score 132; DB 2; Length 1160;
Best Local Similarity 100.0%; Pred. No. 3.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFPGTGGLPGVK 23
Db 196 ERGPPGPGQARGFPGTGGLPGVK 218

RESULT 4
Q7T27 PRELIMINARY; PRT; 1269 AA.
ID Q7T27;
AC Q7T27;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha 1 type II procollagen (Fragment).
GN Name=COL2A1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Caixia X., Yongzhi X., Siqi G., Yuying S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF452711; AAO33039.2; -;
DR GO; GO:0005581; C:collagen; IEA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg helix.
DR InterPro; IPR008160; Collagen.

DR InterPro; IPR008895; Fib.collagen_C.
DR Pfam; PF01410; COLFI; 1.
DR ProDom; PD000007; Clg helix; 17.
DR ProDom; PD002078; Fib.collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
KW Collagen.
FT NON_TER 1
SQ SEQUENCE 1269 AA; 120116 MW; 446EF91BEB8B6A CRC64;

Query Match 100.0%; Score 132; DB 2; Length 1269;
Best Local Similarity 100.0%; Pred. No. 3.6e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFPGTGGLPGVK 23
Db 47 ERGPPGPGQARGFPGTGGLPGVK 69

RESULT 5
CA12_HUMAN STANDARD; PRT; 1418 AA.
ID CA12_HUMAN
AC P02458;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 25-JAN-2005 (Rel. 46, Last annotation update)
DE Collagen alpha 1(II) chain precursor [Contains: Chondrocalcin].
GN Name=COL2A1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90067946; PubMed=2597267;
RA Su M.W., Lee B., Ramirez F., Machado M.A., Horton W.A.;
RT "Nucleotide sequence of the full length cDNA encoding for human type
RT II procollagen.";
RL Nucleic Acids Res. 17:9473-9473(1989).
RN [2]
RP SEQUENCE OF 1-28 FROM N.A., AND VARIANT THR-9.
RX MEDLINE=87031574; PubMed=3021582; DOI=10.1016/0378-1119(86)90037-5;
RA Nunez A.M., Kohno K., Martin G.R., Yamada Y.;
RT "Promoter region of the human pro-alpha 1(II)-collagen gene.";
RL Gene 44:11-16(1986).
RN [3]
RP SEQUENCE OF 432-1145 FROM N.A.
RA Ramirez F.;
RL Submitted (DEC-1988) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 963-1418 FROM N.A.
RX MEDLINE=85190534; PubMed=3857598;
RA Cheah K.S.E., Stoker N.G., Griffin J.R., Grosveld F.G., Solomon E.;
RT "Identification and characterization of the human type II collagen
RT gene (COL2A1).";
RL Proc. Natl. Acad. Sci. U.S.A. 82:2555-2559(1985).
RN [5]
RP SEQUENCE OF 1120-1398 FROM N.A.
RX MEDLINE=85306861; PubMed=3840017;
RA Elina K., Maekelae J.K., Vuorio T., Kauppinen S., Knowles J.,
RA Vuorio E.;
RT "Construction and identification of a cDNA clone for human type II
RT procollagen mRNA";
RL Biochem. J. 229:183-188(1985).
RN [6]
RP SEQUENCE OF 1106-1418 FROM N.A.
RX MEDLINE=88067771; PubMed=2825137;
RA Elina K., Vuorio T., Vuorio E.;
RT "Determination of the single polyadenylation site of the human pro
RT alpha 1(II) collagen gene.";
RL Nucleic Acids Res. 15:9499-9504(1987).
RN [7]
RP SEQUENCE OF 1227-1289 FROM N.A.

RX MEDLINE=86104139; PubMed=3002437;
RA Nunez A.M., Francomano C., Young M.F., Martin G.R., Yamada Y.;
RT "Isolation and partial characterization of genomic clones coding for a
RT human pro-alpha 1 (II) collagen chain and demonstration of restriction
RT fragment length polymorphism at the 3' end of the gene.";
RL Biochemistry 24:6343-6348(1985).
RN [18]
RX SEQUENCE OF 1176-1226 FROM N.A.
RP MEDLINE=84118798; PubMed=6320112;
RA Strom C.M., Upholt W.B.;
RT "Isolation and characterization of genomic clones corresponding to the
RT human type II procollagen gene.";
RL Nucleic Acids Res. 12:1025-1038(1984).
RN [9]
RX SEQUENCE OF 35-167 FROM N.A.
RP MEDLINE=89233138; PubMed=2714801;
RA Su M.W., Benson-Chanda V., Vissing H., Ramirez F.;
RT "Organization of the exons coding for pro alpha 1(II) collagen N-
RT propeptide confirms a distinct evolutionary history of this domain of
RT the fibrillar collagen genes.";
RL Genomics 4:438-441(1989).
RN [10]
RP REVIEW ON VARIANTS
RX MEDLINE=91184577; PubMed=2010058;
RA Kuivaniemi H., Tromp G., Prockop D.J.;
RT "Mutations in collagen genes: causes of rare and some common diseases
RT in humans.";
RL FASEB J. 5:2052-2060(1991).
RN [11]
RP REVIEW ON VARIANTS
RX MEDLINE=97259599; PubMed=9101280;
RA DOI=10.1002/(SICI)1098-1004(1997)9:4<300::AID-HUMU2>3.3.CO;2-8;
RA Kuivaniemi H., Tromp G., Prockop D.J.;
RT "Mutations in fibrillar collagens (types I, II, III, and XI), fibril-
RT associated collagen (type IX), and network-forming collagen (type X)
RT cause a spectrum of diseases of bone, cartilage, and blood vessels.";
RL Hum. Mutat. 9:300-315(1997).
RN [12]
RP VARIANT SER-1074.
RX MEDLINE=90036909; PubMed=2572591;
RA Vissing H., D'Alessio M., Lee B., Ramirez F., Godfrey M.,
RA Hollister D.W.;
RT "Glycine to serine substitution in the triple helical domain of pro-
RT alpha 1 (II) collagen results in a lethal perinatal form of short-
RT limbed dwarfism.";
RL J. Biol. Chem. 264:18265-18267(1989).
RN [13]
RP VARIANT SEDC 1095-GLY--TYR-1330 DEL.
RX MEDLINE=89266907; PubMed=2543071;
RA Lee B., Vissing H., Ramirez F., Rogers D., Rimoin D.L.;
RT "Identification of the molecular defect in a family with
RT spondyloepiphyseal dysplasia.";
RL Science 244:978-980(1989).
RN [14]
RP VARIANT OSTEOARTHRTIS CVS-650.
RX MEDLINE=90370826; PubMed=1975693;
RA Ala-Kokko L., Baldwin C.T., Moskowitz R.W., Prockop D.J.;
RT "Single base mutation in the type II procollagen gene (COL2A1) as a
RT cause of primary osteoarthritis associated with a mild
RT chondrodysplasia.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6565-6568(1990).
RN [15]
RP VARIANT OSTEOARTHRTIS CVS-650.
RX MEDLINE=91086471; PubMed=1985108;
RA Eyre D.R., Weis M.A., Moskowitz R.W.;
RT "Cartilage expression of a type II collagen mutation in an inherited
RT form of osteoarthritis associated with a mild chondrodysplasia.";
RL J. Clin. Invest. 87:357-361(1991).
RN [16]
RP VARIANT HYPOCHONDROGENESIS GLU-984.
RX MEDLINE=93054548; PubMed=1429602;
RA Bogert R., Tiller G.E., Wies M.A., Gruber H.E., Rimoin D.L.,
RA Cohn D.H., Eyre D.R.;
RT "An amino acid substitution (Gly853-->Glu) in the collagen alpha 1(II)
RT chain produces hypochondrogenesis.";
RL J. Biol. Chem. 267:22522-22526(1992).
RN [17]
RP VARIANT HYPOCHONDROGENESIS SER-705.
RX MEDLINE=92262484; PubMed=1374906;
RA Horton W.A., Machado M.A., Ellard J., Campbell D., Bartley J.,
RA Ramirez F., Vitale E., Lee B.;
RT "Characterization of a type II collagen gene (COL2A1) mutation
RT identified in cultured chondrocytes from human hypochondrogenesis.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4583-4587(1992).
RN [18]
RP VARIANT WS-II ASP-198.
RX MEDLINE=93304428; PubMed=8317498;
RA Koerkoe J., Ritvaniemi P., Haataja L., Kaeerlaeinen H.,
RA Kivirikko K.I., Prockop D.J., Ala-Kokko L.;
RT "Mutation in type II procollagen (COL2A1) that substitutes aspartate
RT for glycine alpha 1-67 and that causes cataracts and retinal
RT detachment: evidence for molecular heterogeneity in the Wagner
RT syndrome and the Stickler syndrome (arthro-ophthalmopathy).";
RL Am. J. Hum. Genet. 53:55-61(1993).
RN [19]
RP VARIANT SEMD CYS-840.
RX MEDLINE=93252400; PubMed=8486375;
RA Tiller G.E., Weis M.A., Lachman R.S., Cohn D.H., Rimoin D.L.,
RA Eyre D.R.;
RT "A dominant mutation in the type II collagen gene (COL2A1) produces
RT spondyloepimetaphyseal dysplasia (SEMD), Strudwick type.";
RL Am. J. Hum. Genet. 53:A209-A209(1993).
RN [20]
RP VARIANT OSTEOARTHRTIS CVS-650.
RX MEDLINE=93282819; PubMed=8507190;
RA Holderbaum D., Malesud C.J., Moskowitz R.W., Haqqi T.M.;
RT "Human cartilage from late stage familial osteoarthritis transcribes
RT type II collagen mRNA encoding a cysteine in position 519.";
RL Biochem. Biophys. Res. Commun. 192:1169-1174(1993).
RN [21]
RP VARIANT SEMD ARG-285.
RX MEDLINE=93252400; PubMed=8486375;
RA Vikkula M., Ritvaniemi P., Vuorio A.F., Kaitila I., Ala-Kokko L.,
RA Peltonen L.;
RT "A mutation in the amino-terminal end of the triple helix of type II
RT collagen causing severe osteochondrodysplasia.";
RL Genomics 16:282-285(1993).
RN [22]
RP VARIANT SEDC CYS-206.
RX MEDLINE=94063862; PubMed=8244341;
RA Williams C.J., Considine E.L., Knowlton R.G., Reginato A., Neumann G.,
RA Harrison D., Buxton P., Jimenez S.A., Prockop D.J.;
RT "Spondyloepiphyseal dysplasia and precocious osteoarthritis in a
RT family with an Arg75-->Cys mutation in the procollagen type II gene
RT (COL2A1).";
RL Hum. Genet. 92:499-505(1993).
RN [23]
RP VARIANT SEDC CYS-920.
RX MEDLINE=93315508; PubMed=8325895;
RA Chan D., Taylor T.K.F., Cole W.G.;
RT "Characterization of an arginine 789 to cysteine substitution in alpha
RT 1 (II) collagen chains of a patient with spondyloepiphyseal
RT dysplasia.";
RL J. Biol. Chem. 268:15238-15245(1993).
RN [24]
RP VARIANT SEDC SER-1128.
RX MEDLINE=93140139; PubMed=8423604;
RA Cole W.G., Hall R.K., Rogers J.G.;
RT "The clinical features of spondyloepiphyseal dysplasia congenita
RT resulting from the substitution of glycine 997 by serine in the alpha
RT 1(II) chain of type II collagen.";
RL J. Med. Genet. 30:27-35(1993).
RN [25]
RP VARIANT STU1 233-ALA--LYS-239 DEL.
RX MEDLINE=95067975; PubMed=7977371;
RA Bogert R., Wilkin D.J., Wilcox W.R., Lachman R.S., Rimoin D.L.,
RA Cohn D.H., Eyre D.R.;


```
RT "Expression, in cartilage, of a 7-amino-acid deletion in type II
RT collagen from two unrelated individuals with Knieset dysplasia.";
Query Match 100.0%; Score 132; DB 1; Length 1418;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGLPGVK 23
   |||||
Db 196 ERGPPGPGQARGPFGTGLPGVK 218

RESULT 6
Q28396 PRELIMINARY; PRT; 1418 AA.
AC Q28396;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Type II collagen.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97350165; PubMed=9205943; DOI=10.1016/S0945-053X(97)90073-1;
RA Richardson D.W., Dodge G.R.;
RT "Cloning of equine type II procollagen and the modulation of its
RT expression in cultured equine articular chondrocytes.";
RL Matrix Biol. 16:59-64(1997).
DR EMBL; U62528; AAB05773.1; -.
DR PIR; T45467;
DR GO; GO:0005581; C:collagen; IEA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008885; Fib_collagen_C.
DR Pfam; PF01410; COLFI; 1.
DR Pfam; PF01391; Collagen; 18.
DR ProDom; PD000007; Clg helix; 5.
DR ProDom; PD002078; Fib_collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
KW Collagen.
SQ SEQUENCE 1418 AA; 134343 MW; 115FCD19B86596A3 CRC64;

Query Match 100.0%; Score 132; DB 2; Length 1418;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGLPGVK 23
   |||||
Db 196 ERGPPGPGQARGPFGTGLPGVK 218

RESULT 7
Q9W7R9 PRELIMINARY; PRT; 1418 AA.
AC Q9W7R9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Alpha type II collagen.
OS Cynops pyrrhogaster (Japanese common newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.
OX NCBI_TaxID=8330;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99407244; PubMed=10474166;
RX DOI=10.1002/(STCI)1097-0177(199909)216:1<59::AID-DVDY8>3.3.CO;2-2;
```

```
RA Asahina K., Obara M., Yoshizato K.;
RT "Expression of genes of type I and type II collagen in the formation
RT and development of the blastema of regenerating newt limb.";
RL Dev. Dyn. 216:59-71(1999).
DR EMBL; AB022046; BAA82043.1; -.
DR GO; GO:0005581; C:collagen; IEA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR008885; Fib_collagen_C.
DR Pfam; PF01410; COLFI; 1.
DR Pfam; PF01391; Collagen; 18.
DR ProDom; PD000007; Clg helix; 7.
DR ProDom; PD002078; Fib_collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
KW Collagen.
SQ SEQUENCE 1418 AA; 135066 MW; C19A6E601A2A717E CRC64;

Query Match 100.0%; Score 132; DB 2; Length 1418;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGLPGVK 23
   |||||
Db 196 ERGPPGPGQARGPFGTGLPGVK 218

RESULT 8
Q9W37 PRELIMINARY; PRT; 1420 AA.
AC Q9W37;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Alpha 1 type IIA collagen precursor.
GN Name=COL2A1;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Sternal;
RA Caixia X., Yongzhi X., Siqi G., Yiyang S.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY046949; AAK98621.1; -.
DR GO; GO:0005581; C:collagen; IEA.
DR GO; GO:0005737; C:cytoplasm; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR Pfam; PF01410; COLFI; 1.
DR Pfam; PF01391; Collagen; 18.
DR ProDom; PD000007; Clg helix; 7.
DR ProDom; PD002078; Fib_collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
KW Collagen; Signal.
FT SIGNAL
SQ SEQUENCE 1420 AA; 134998 MW; 88D9AAB17F214FF5 CRC64;

Query Match 100.0%; Score 132; DB 2; Length 1420;
Best Local Similarity 100.0%; Pred. No. 4e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGLPGVK 23
   |||||
Db 198 ERGPPGPGQARGPFGTGLPGVK 220

RESULT 9
Q91717
```

RA	Raha S.S., Loquellano N.A., Peters G.J., Abranson R.D., Mullaby S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.B., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RT	[2]
RN	SEQUENCE FROM N.A.
RN	TISSUE=Embryo;
RC	MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RX	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.; "Genetic and genomic tools for Xenopus research: The NIH Xenopus initiative."
RA	Dev. Dyn. 225:384-391(2002).
RT	[3]
RN	SEQUENCE FROM N.A.
RN	TISSUE=Embryo;
RC	Klein S., Strausberg R.; Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RA	EMBL; BC048221; AAH48221.1; "
DR	GO; GO:0005581; C:collagen; IEA.
DR	GO; GO:0005737; C:cyclopia; IEA.
DR	GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR	GO; GO:0006817; P:phosphate transport; IEA.
DR	InterPro; IPR008161; Clg helix.
DR	InterPro; IPR008160; Collagen.
DR	InterPro; IPR000885; Fib collagen_C.
DR	InterPro; IPR009041; WPC_SGCI.
DR	InterPro; IPR001007; FMP CCl.
DR	Pfam; PF01410; COLFI; 1.
DR	Pfam; PF01391; Collagen; 18.
DR	Pfam; PF00093; VWC; 1.
DR	ProDom; PD000007; Clg_helix; 7.
DR	ProDom; PD002078; Fib_collagen_C; 1.
DR	SMART; SM00038; COLFI; 1.
DR	SMART; SM00214; VMC; 1.
DR	PROSITE; PS01208; VWFC_1; 1.
DR	PROSITE; PS50184; VWFC_2; 1.
DR	Collagen.
KN	SEQUENCE 1486 AA; 142263 MW; 02C18E5F5807100E CRC64;
SQ	Query Match 100.0%; Score 132; DB 2; Length 1486; Best Local Similarity 100.0%; Pred.No. 4.1e-07; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps
Qy	1 ERGPFGQGARGFGTPTGLPGVK 23
Dd	267 ERGPFGQGARGFGTPTGLPGVK 289
RESULT 11	
ID Q14047	PRELIMINARY; PRT; 1487 AA.
DT Q14047	
AC 01-NOV-1996	(TrEMBLrel. 01, Created)
DT 01-NOV-1996	(TrEMBLrel. 01, Last sequence update)
DE 01-JUN-2003	(TrEMBLrel. 24, Last annotation update)
DI Alpha-1 type II collagen.	
GN Names=COL2A1;	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX NCBI_Taxid=9606;	
RN [1]	
RN RP	SEQUENCE FROM N.A.

RC TISSUE=Blood;
RX MEDLINE=85190534; PubMed=3857598;
RA Cheah K.S., Stoker N.G., Griffin J.R., Grosveld F.G., Solomon E.;
RT "Identification and characterization of the human type II collagen
gene (COL2A1).";
RL Proc. Natl. Acad. Sci. U.S.A. 82:2555-2559(1985).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RC MEDLINE=90026318; PubMed=2803268;
RA Baldwin C.T., Reginato A.M., Smith C., Jimenez S.A., Prockop D.J.;
RT "Structure of cDNA clones coding for human type II procollagen. The
alpha 1(II) chain is more similar to the alpha 1(I) chain than two
other alpha chains of fibrillar collagens.";
RL Biochem. J. 262:521-528(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RC MEDLINE=89325561; PubMed=2753125; DOI=10.1016/0014-5793(89)80713-6;
RA Vikkula M., Peltonen L.;
RT "Structural analyses of the polymorphic area in type II collagen
gene.";
RL FEBS Lett. 250:171-174(1989).
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RC MEDLINE=91184811; PubMed=2081599;
RA Ryan M.C., Sieraski M., Sandell L.J.;
RT "The human type II procollagen gene: identification of an additional
protein-coding domain and location of potential regulatory sequences
in the promoter and first intron.";
RL Genomics 8:41-48(1990).
RN [5]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RC MEDLINE=91153296; PubMed=1999183;
RA Huang M.C., Seyer J.M., Thompson J.P., Spinella D.G., Cheah K.S.,
RA* Kang A.H.;
RT "Genomic organization of the human procollagen alpha 1(II) collagen
gene.";
RL Eur. J. Biochem. 195:593-600(1991).
RN [6]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RC MEDLINE=92344585; PubMed=1637314;
RA Vikkula M., Metsaranta M., Syvanen A.C., Ala-Kokko L., Vuorio E.,
RA Peltonen L.;
RT "Structural analysis of the regulatory elements of the type-II
procollagen gene. Conservation of promoter and first intron sequences
between human and mouse.";
RL Biochem. J. 285:0-0(0).
RN [7]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RC MEDLINE=97104294; PubMed=8948452;
RA Ala-Kokko L., Kvist A.P., Metsaranta M., Kivirikko K.I.,
RA de Crombrughe B., Prockop D.J., Vuorio E.;
RT "Conservation of the sizes of 5' introns and over 100 intronic
sequences for the binding of common transcription factors in the human
and mouse genes for type II procollagen (COL2A1).";
RL Biochem. J. 308:0-0(0).
DR EMBL; L10347; AAC41772.1; -;
DR GO; GO:0005581; C:collagen; IEA.
DR GO; GO:0005737; C:cyclopasim; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR000885; Fib_collagen_C.
DR InterPro; IPR009041; PMP_SGCI.
DR Pfam; PF01410; COLFI; 1.
DR Pfam; PF01391; Collagen; 18.
DR Pfam; PF00093; VMC; 1.
DR Pfam; PF01391; Collagen; 18.
DR ProDom; PD000007; Clg_helix; 5.
DR ProDom; PD0002078; Fib_collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
DR SMART; SM00214; VMC; 1.
DR PROSITE; PS01208; VWFC_1; 1.
DR PROSITE; PS0184; VWFC_2; 1.
KW Collagen.
SQ SEQUENCE 1487 AA; 141874 MW; 25873EAC1E311DB8 CRC64;
Query Match 100.0%; Score 132; DB 2; Length 1487;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RY 1 ERGPPGPGQARGFGTGTGLPGVK 23
|||||
DB 265 ERGPPGPGQARGFGTGTGLPGVK 287

DR Pfam; PF00093; VMC; 1.
DR ProDom; PD000007; Clg_helix; 6.
DR ProDom; PD002078; Fib_collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
DR SMART; SM00214; VMC; 1.
DR PROSITE; PS01208; VWFC_1; 1.
DR PROSITE; PS0184; VWFC_2; 1.
KW Collagen.
SQ SEQUENCE 1487 AA; 141771 MW; 0B7E79D46BDAFA97 CRC64;
Query Match 100.0%; Score 132; DB 2; Length 1487;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ERGPPGPGQARGFGTGTGLPGVK 23
|||||
DB 265 ERGPPGPGQARGFGTGTGLPGVK 287

RESULT 12
O7753
ID O7753 PRELIMINARY; PRT; 1487 AA.
AC O7753;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Type IIA procollagen.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98340920; PubMed=9676231;
Du F., Acland G.M., Ray J.;
RT "Differential splicing of type II procollagen mRNA in canine retina.";
RL Anim. Biotechnol. 9:15-20(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20480698; PubMed=11024291; DOI=10.1016/S0378-1119(00)00324-3;
Du F., Acland G.M., Ray J.;
RT "Cloning and expression of type II collagen mRNA: evaluation as a
candidate for canine oculo-skeletal dysplasia.";
RL Gene 255:307-316(2000).
DR EMBL; AF023169; AAC62178.2; -;
DR GO; GO:0005581; C:collagen; IEA.
DR GO; GO:0005737; C:cyclopasim; IEA.
DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
DR GO; GO:0006817; P:phosphate transport; IEA.
DR InterPro; IPR008161; Clg_helix.
DR InterPro; IPR008160; Collagen.
DR InterPro; IPR000885; Fib_collagen_C.
DR InterPro; IPR009041; PMP_SGCI.
DR InterPro; IPR001007; VWFC_C.
DR Pfam; PF01410; COLFI; 1.
DR Pfam; PF01391; Collagen; 18.
DR Pfam; PF00093; VMC; 1.
DR ProDom; PD000007; Clg_helix; 5.
DR ProDom; PD0002078; Fib_collagen_C; 1.
DR SMART; SM00038; COLFI; 1.
DR SMART; SM00214; VMC; 1.
DR PROSITE; PS01208; VWFC_1; 1.
DR PROSITE; PS0184; VWFC_2; 1.
KW Collagen.
SQ SEQUENCE 1487 AA; 141874 MW; 25873EAC1E311DB8 CRC64;
Query Match 100.0%; Score 132; DB 2; Length 1487;
Best Local Similarity 100.0%; Pred. No. 4.1e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ERGPPGPGQARGFGTGTGLPGVK 23
|||||
DB 265 ERGPPGPGQARGFGTGTGLPGVK 287

RESULT 13
 Q91718 PRELIMINARY; PRT; 1491 AA.
 ID Q91718; PRT; 1491 AA.
 AC Q91718; PRT; 1491 AA.
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Alpha-1 type II' collagen
 GN Name=alpha-1 type II' collagen;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92011898; PubMed=1918153; DOI=10.1083/jcb.115.2.565;
 RA Su M.W., Suzuki H.R., Bieker J.J., Solursh M., Ramirez F.;
 RT "Expression of two nonallelic type II procollagen genes during Xenopus
 RT laevis embryogenesis is characterized by stage-specific production of
 RT alternatively spliced transcripts.";
 RL J. Cell Biol. 115:565-575(1991).
 DR EMBL; M63596; AAA49679.1; -;
 DR PIR; A40333; A40333.
 DR PIR; B40333; B40333.
 DR GO; GO:0005581; C:collagen; IEA.
 DR GO; GO:0005737; C:cycloplasm; IEA.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
 DR GO; GO:0006817; P:phosphate transport; IEA.
 DR Pfam; PF01410; COLFI; 1.
 DR Pfam; PF01391; Collagen; 18.
 DR Pfam; PF00093; VWC; 1.
 DR ProDom; PD000007; Clg_helix; 4.
 DR ProDom; PD002078; Fib_collagen_C; 1.
 DR SMART; SM00038; COLFI; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS01208; VWFC_1; 1.
 DR PROSITE; PS0184; VWFC_2; 1.
 KW Collagen.
 SQ SEQUENCE 1491 AA; 142495 MW; 43026FF08FB0314 CRC64;
 Query Match 100.0%; Score 132; DB 2; Length 1491;
 Best Local Similarity 100.0%; Pred. No. 4.1e-07;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ERGPPGPGARGFPPTGLPGVK 23
 Db 270 ERGPPGPGARGFPPTGLPGVK 292
 |||||
 RESULT 14
 Q72TM4 PRELIMINARY; PRT; 1491 AA.
 ID Q72TM4; PRT; 1491 AA.
 AC Q72TM4; PRT; 1491 AA.
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE LOC397739 protein.
 GN Names=LOC397739;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Embryo;
 MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Embryo;
 MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC044962; AAA44962.1; -;
 DR GO; GO:0005581; C:collagen; IEA.
 DR GO; GO:0005737; C:cycloplasm; IEA.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
 DR GO; GO:0006817; P:phosphate transport; IEA.
 DR InterPro; IPR008161; Clg_helix.
 DR InterPro; IPR008160; Collagen.
 DR InterPro; IPR00885; Fib_collagen_C.
 DR InterPro; IPR009041; PMP_SGCI.
 DR InterPro; IPR001007; VWFC_
 DR Pfam; PF01410; COLFI; 1.
 DR Pfam; PF01391; Collagen; 18.
 DR Pfam; PF00093; VWC; 1.
 DR ProDom; PD000007; Clg_helix; 4.
 DR ProDom; PD002078; Fib_collagen_C; 1.
 DR SMART; SM00038; COLFI; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS01208; VWFC_1; 1.
 DR PROSITE; PS0184; VWFC_2; 1.
 KW Collagen.
 SQ SEQUENCE 1491 AA; 142492 MW; 2FF7A8DE36D73BC1 CRC64;
 Query Match 100.0%; Score 132; DB 2; Length 1491;
 Best Local Similarity 100.0%; Pred. No. 4.1e-07;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ERGPPGPGARGFPPTGLPGVK 23
 Db 270 ERGPPGPGARGFPPTGLPGVK 292
 |||||
 RESULT 15
 Q6P4Z2 PRELIMINARY; PRT; 1492 AA.
 ID Q6P4Z2; PRT; 1492 AA.
 AC Q6P4Z2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein MGC75588.
 GN Names=MGC75588;
 OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8364;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
 Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Gerhard D.S.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC063191; AAH63191.1; -;
 DR GO; GO:0005581; C:collagen; IEA.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0005201; F:extracellular matrix structural constituent; IEA.
 DR GO; GO:0006817; P:phosphate transport; IEA.
 DR InterPro; IPR008161; Clg helix.
 DR InterPro; IPR008160; Collagen.
 DR InterPro; IPR000885; Fib_collagen_C.
 DR InterPro; IPR009041; FMP_SGCI.
 DR InterPro; IPR001007; VWF_C.
 DR Pfam; PF01410; COLFI; 1.
 DR Pfam; PF00093; VWC; 1.
 DR ProDom; PD000007; Clg_helix; 7.
 DR ProDom; PD002078; Fib_collagen_C; 1.
 DR SMART; SM00038; COLFI; 1.
 DR SMART; SM00214; VWC; 1.
 DR PROSITE; PS01208; VWF_C; 1.
 DR PROSITE; PS0184; VWF_C; 1.
 KW Collagen; Hypothetical protein.
 SQ SEQUENCE 1492 AA; 142696 MW; DB7AF42B94210EB7 CRC64;
 Query Match 100.0%; Score 132; DB 2; Length 1492;
 Best Local Similarity 100.0%; Pred. No. 4, 1e-07;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGQARGFGTGLPGVK 23
 Db 270 ERGPPGQARGFGTGLPGVK 292

Search completed: October 8, 2005, 00:26:38
 Job time : 178 secs

This Page Blank (uspio)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2005, 00:21:07 ; Search time 41 Seconds
(without alignments)
41.876 Million cell updates/sec

Title: US-10-674-065-3

Perfect score: 132

Sequence: 1 ERGPPGQARGFGPTGPGVK 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/prodata/1/iaa/5A COMB.pcp.*

2: /cgn2_6/prodata/1/iaa/5B COMB.pcp.*

3: /cgn2_6/prodata/1/iaa/6A COMB.pcp.*

4: /cgn2_6/prodata/1/iaa/6B COMB.pcp.*

5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pcp.*

6: /cgn2_6/prodata/1/iaa/backfiles1.pcp.*

* Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	492	4	US-08-468-996-11
2	132	100.0	1017	4	US-08-468-996-10
3	132	100.0	1060	3	US-08-931-820-3
4	132	100.0	1418	3	US-08-963-825-20
5	132	100.0	1418	3	US-09-010-999-1
6	132	100.0	1418	3	US-09-500-811-20
7	132	100.0	1418	3	US-09-570-573-20
8	132	100.0	1418	3	US-09-548-608-20
9	117	88.6	1442	2	US-08-316-650-12
10	117	88.6	1442	5	PCT-US95-02251-12
11	115	87.1	310	3	US-09-219-849-47
12	115	87.1	492	4	US-08-468-996-12
13	115	87.1	595	3	US-09-219-849-48
14	115	87.1	595	3	US-09-219-849-50
15	115	87.1	822	3	US-09-219-849-49
16	115	87.1	1057	4	US-08-931-820-1
17	115	87.1	1461	4	US-09-585-887-9
18	115	87.1	1461	4	US-09-289-578-9
19	115	87.1	1464	4	US-09-331-347C-21
20	112	84.8	1341	3	US-08-963-825-18
21	112	84.8	1341	3	US-09-500-811-18
22	112	84.8	1341	3	US-09-570-573-18
23	112	84.8	1341	3	US-09-548-608-18
24	109	82.6	684	4	US-09-949-016-8348
25	109	82.6	1024	3	US-08-931-820-2
26	109	82.6	1366	3	US-08-963-825-19
27	109	82.6	1366	3	US-09-500-811-19

28	109	82.6	1366	3	US-09-570-573-19	Sequence 19, Appl
29	109	82.6	1366	3	US-09-548-608-19	Sequence 19, Appl
30	109	82.6	1366	4	US-09-585-887-10	Sequence 10, Appl
31	109	82.6	1366	4	US-09-289-578-10	Sequence 10, Appl
32	109	82.6	1366	4	US-09-949-016-5882	Sequence 5882, Ap
33	92	69.7	546	1	US-08-494-168-10	Sequence 10, Appl
34	92	69.7	1218	4	US-09-949-016-7065	Sequence 7065, Ap
35	92	69.7	1268	4	US-09-949-016-7487	Sequence 7487, Ap
36	92	69.7	1690	4	US-09-949-016-5884	Sequence 5884, Ap
37	91	68.9	938	4	US-09-949-016-9992	Sequence 9992, Ap
38	90	68.2	489	2	US-08-794-795-7	Sequence 7, Appli
39	90	68.2	489	3	US-09-249-200-7	Sequence 7, Appli
40	90	68.2	518	1	US-08-392-367B-2	Sequence 2, Appli
41	90	68.2	518	3	US-08-893-467A-2	Sequence 2, Appli
42	88	66.7	755	4	US-09-919-497-57	Sequence 57, Appl
43	87	65.9	228	3	US-09-219-849-38	Sequence 38, Appl
44	87	65.9	260	4	US-09-949-016-11119	Sequence 11119, A
45	87	65.9	377	3	US-09-342-681C-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-08-468-996-11

; Sequence 11, Application US/08468996

; Patent No. 6645504

; GENERAL INFORMATION:

; APPLICANT: Weiner, Howard

; APPLICANT: Miller, Ariel

; APPLICANT: Zheng, Zheng

; APPLICANT: Ahmad, Al-Sabbagh

; TITLE OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION

; TITLE OF INVENTION: GLUCAGON

; FILE REFERENCE: 1010/18959-US3

; CURRENT APPLICATION NUMBER: US/08/468,996

; CURRENT FILING DATE: 2003-02-07

; PRIOR APPLICATION NUMBER: US 07/843,752

; PRIOR FILING DATE: 1992-02-28

; PRIOR APPLICATION NUMBER: US 07/460,852

; PRIOR FILING DATE: 1990-02-21

; PRIOR APPLICATION NUMBER: US 07/596,936

; PRIOR FILING DATE: 1990-10-15

; PRIOR APPLICATION NUMBER: US 07/065,734

; PRIOR FILING DATE: 1987-06-24

; PRIOR APPLICATION NUMBER: US 07/454,486

; PRIOR FILING DATE: 1989-12-20

; PRIOR APPLICATION NUMBER: US 07/487,732

; PRIOR FILING DATE: 1990-03-02

; PRIOR APPLICATION NUMBER: US 07/551,632

; PRIOR FILING DATE: 1990-07-10

; PRIOR APPLICATION NUMBER: US 07/379,778

; PRIOR FILING DATE: 1989-07-14

; PRIOR APPLICATION NUMBER: US 07/607,826

; PRIOR FILING DATE: 1990-10-31

; PRIOR APPLICATION NUMBER: US 07/595,468

; PRIOR FILING DATE: 1990-10-10

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 11

; LENGTH: 492

; TYPE: PRT

; ORGANISM: Bos taurus

US-08-468-996-11

Query Match 100.0%; Score 132; DB 4; Length 492;

Best Local Similarity 100.0%; Pred. No. 1.4e-08;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGQARGFGPTGPGVK 23

65 ERGPPGQARGFGPTGPGVK 87

DB

Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPPTGGLPGVK 23
Db 196 ERGPPGPGQARGPPTGGLPGVK 218

RESULT 5
US-09-010-999-1
; Sequence 1, Application US/09010999
; Patent No. 6132976
; GENERAL INFORMATION:
; APPLICANT: Poole, Anthony R.
; APPLICANT: Hollander, Anthony P.
; APPLICANT: Billingham, R. C.
; TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
; TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,999
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 4335
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,501
; FILING DATE: 17-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/984,123
; FILING DATE: 04-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 032931/0212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human Type II Collagen

US-09-010-999-1
Query Match 100.0%; Score 132; DB 3; Length 1418;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPPTGGLPGVK 23
Db 196 ERGPPGPGQARGPPTGGLPGVK 218

RESULT 6
US-09-500-811-20
; Sequence 20, Application US/09500811
; Patent No. 6323314
; GENERAL INFORMATION:
; APPLICANT: Poole, Anthony R.
; APPLICANT: Hollander, Anthony P.
; APPLICANT: Billingham, R. C.
; TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
; TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,999
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 4335
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,501
; FILING DATE: 17-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/984,123
; FILING DATE: 04-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 032931/0212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human Type II Collagen

US-09-010-999-1
Query Match 100.0%; Score 132; DB 3; Length 1418;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPPTGGLPGVK 23
Db 196 ERGPPGPGQARGPPTGGLPGVK 218

RESULT 7
US-09-570-573-20
; Sequence 20, Application US/09570573
; Patent No. 6342361
; GENERAL INFORMATION:
; APPLICANT: Poole, Anthony R.
; APPLICANT: Hollander, Anthony P.
; APPLICANT: Billingham, R. C.
; TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
; TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,999
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 4335
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,501
; FILING DATE: 17-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/984,123
; FILING DATE: 04-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 032931/0212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human Type II Collagen

US-09-570-573-20
Query Match 100.0%; Score 132; DB 3; Length 1418;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPPTGGLPGVK 23
Db 196 ERGPPGPGQARGPPTGGLPGVK 218

RESULT 8
US-09-500-811-20
; Sequence 20, Application US/09500811
; Patent No. 6323314
; GENERAL INFORMATION:
; APPLICANT: Poole, Anthony R.
; APPLICANT: Hollander, Anthony P.
; APPLICANT: Billingham, R. C.
; TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
; TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,999
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 4335
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,501
; FILING DATE: 17-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/984,123
; FILING DATE: 04-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 032931/0212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human Type II Collagen

US-09-500-811-20
Query Match 100.0%; Score 132; DB 3; Length 1418;
Best Local Similarity 100.0%; Pred. No. 3.9e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPPTGGLPGVK 23
Db 196 ERGPPGPGQARGPPTGGLPGVK 218

RESULT 9
US-09-570-573-20
; Sequence 20, Application US/09570573
; Patent No. 6342361
; GENERAL INFORMATION:
; APPLICANT: Poole, Anthony R.
; APPLICANT: Hollander, Anthony P.
; APPLICANT: Billingham, R. C.
; TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
; TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/010,999
; FILING DATE: 22-JAN-1998
; CLASSIFICATION: 4335
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/448,501
; FILING DATE: 17-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/984,123
; FILING DATE: 04-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 032931/0212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Human Type II Collagen

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Gogoris, Adda C
; REGISTRATION NUMBER: 29,714
; REFERENCE/DOCKET NUMBER: 4305/08701
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-527-7700
; TELEFAX: 212-753-6237
; TELEX: 236687
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1418 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; IMMEDIATE SOURCE:
; CLONE: COLLAGEN -ALPHA 1 (II)
; US-09-548-608-20

Query Match 100.0%; Score 132; DB 3; Length 1418;
Best Local Similarity 100.0%; Pred.No.3.9e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0

QY 1 ERGPPGQGARGFGTGLPGVK 23
   |||||
Db 196 ERGPPGQGARGFGTGLPGVK 218

RESULT 9
US-08-316-650-12
; Sequence 12, Application US/08316650
; Patent No. 5942496
; GENERAL INFORMATION:
; APPLICANT: Bonadio, Jeffrey
; APPLICANT: Roessler, Blake J.
; APPLICANT: Goldstein, Steven A.
; APPLICANT: Lin, Wushan
; TITLE OF INVENTION: METHODS AND COMPOSITIONS
; TITLE OF INVENTION: FOR STIMULATING BONE CELLS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/316,650
; FILING DATE: 30-SEP-1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/199,780
; FILING DATE: 30-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, David L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UMIC:008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1442 amino acids
; TYPE: amino acid

```

RESULT 11

NUMBER OF SEO ID NOS: 13

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 492
; TYPE: PRT
; ORGANISM: Bos taurus
US-08-468-996-12

Query Match      87.1%; Score 115; DB 4; Length 492;
Best Local Similarity 87.0%; Pred. No. 1.6e-06;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFPPTGTLPGVK 23
Db 65 ERGPPGPGQARGLPGTAGLPGMK 87

RESULT 13
US-09-219-849-48
; Sequence 48, Application US/09219849
; Patent No. 6150081
; GENERAL INFORMATION:
; APPLICANT: VAN HEERDE, GEORGE V.
; APPLICANT: VAN RIJN, ALEXIS C.
; APPLICANT: BOWMSTRA, JAN B.
; APPLICANT: DE WOLF, FREDERIK A.
; APPLICANT: MOOBROEK, ANDREAS
; APPLICANT: WERTEN, MARC W.T.
; APPLICANT: WIND, RICHEL D.
; APPLICANT: VAN DEN BOSCH, TANJA J.
; TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
; TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
; FILE OF INVENTION: PREPARATION THEREOF
; FILE REFERENCE: 2728-2
; CURRENT APPLICATION NUMBER: US/09/219,849
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; TYPE: PRT
; LENGTH: 595
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: amino acid sequence
US-09-219-849-48

Query Match      87.1%; Score 115; DB 3; Length 595;
Best Local Similarity 87.0%; Pred. No. 2e-06;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFPPTGTLPGVK 23
Db 64 ERGPPGPGQARGLPGTAGLPGMK 86

RESULT 14
US-09-219-849-50
; Sequence 50, Application US/09219849
; Patent No. 6150081
; GENERAL INFORMATION:
; APPLICANT: VAN HEERDE, GEORGE V.
; APPLICANT: VAN RIJN, ALEXIS C.
; APPLICANT: BOWMSTRA, JAN B.
; APPLICANT: DE WOLF, FREDERIK A.
; APPLICANT: MOOBROEK, ANDREAS
; APPLICANT: WERTEN, MARC W.T.
; APPLICANT: WIND, RICHEL D.
; APPLICANT: VAN DEN BOSCH, TANJA J.
; TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
; TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
; FILE OF INVENTION: PREPARATION THEREOF
; FILE REFERENCE: 2728-2
; CURRENT APPLICATION NUMBER: US/09/219,849
```

```
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: amino acid sequence
US-09-219-849-50

Query Match      87.1%; Score 115; DB 3; Length 595;
Best Local Similarity 87.0%; Pred. No. 2e-06;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFPPTGTLPGVK 23
Db 64 ERGPPGPGQARGLPGTAGLPGMK 86

RESULT 15
US-09-219-849-49
; Sequence 49, Application US/09219849
; Patent No. 6150081
; GENERAL INFORMATION:
; APPLICANT: VAN HEERDE, GEORGE V.
; APPLICANT: VAN RIJN, ALEXIS C.
; APPLICANT: BOWMSTRA, JAN B.
; APPLICANT: DE WOLF, FREDERIK A.
; APPLICANT: MOOBROEK, ANDREAS
; APPLICANT: WERTEN, MARC W.T.
; APPLICANT: WIND, RICHEL D.
; APPLICANT: VAN DEN BOSCH, TANJA J.
; TITLE OF INVENTION: SILVER HALIDE EMULSIONS WITH RECOMBINANT COLLAGEN
; TITLE OF INVENTION: SUITABLE FOR PHOTOGRAPHIC APPLICATION AND ALSO THE
; FILE OF INVENTION: PREPARATION THEREOF
; FILE REFERENCE: 2728-2
; CURRENT APPLICATION NUMBER: US/09/219,849
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; TYPE: PRT
; LENGTH: 822
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: amino acid sequence
US-09-219-849-49

Query Match      87.1%; Score 115; DB 3; Length 822;
Best Local Similarity 87.0%; Pred. No. 2.7e-06;
Matches 20; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGFPPTGTLPGVK 23
Db 64 ERGPPGPGQARGLPGTAGLPGMK 86

Search completed: October 8, 2005, 00:31:02
Job time : 42 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 8, 2005, 00:17:47 ; Search time 166 Seconds
(without alignments)
57.641 Million cell updates/sec

Title: US-10-674-065-3

Perfect score: 132

Sequence: 1 ERGPPGQAGFGPGTGLPGVK 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1854112 segs, 416015017 residues

Total number of hits satisfying chosen parameters: 1854112

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	23	16	US-10-674-065-3
2	132	100.0	24	16	US-10-674-065-6
3	132	100.0	24	16	US-10-674-065-7
4	132	100.0	24	16	US-10-674-065-8
5	132	100.0	24	16	US-10-674-065-9
6	132	100.0	24	16	US-10-674-065-13
7	132	100.0	24	16	US-10-674-065-14
8	132	100.0	84	16	US-10-674-065-1
9	132	100.0	84	16	US-10-674-065-18
10	132	100.0	85	16	US-10-674-065-11
11	132	100.0	85	16	US-10-674-065-12

12	132	100.0	243	16	US-10-723-860-1085	Sequence 1085, Ap
13	132	100.0	492	16	US-10-639-286-11	Sequence 11, Appl
14	132	100.0	1014	14	US-10-194-441A-1	Sequence 1, Appli
15	132	100.0	1017	16	US-10-639-286-10	Sequence 10, Appl
16	132	100.0	1418	14	US-10-058-124-20	Sequence 20, Appl
17	132	100.0	1418	16	US-10-468-091-5	Sequence 5, Appli
18	132	100.0	1487	18	US-10-756-1419-4739	Sequence 4739, Ap
19	132	100.0	1487	14	US-10-194-441A-48	Sequence 48, Appl
20	132	100.0	1487	16	US-10-468-091-6	Sequence 6, Appli
21	132	100.0	1487	14	US-10-232-175-15	Sequence 15, Appl
22	132	100.0	1487	14	US-10-232-175-16	Sequence 16, Appl
23	132	100.0	1487	14	US-10-342-331-47	Sequence 47, Appl
24	132	100.0	1487	16	US-10-639-286-12	Sequence 12, Appl
25	132	100.0	1487	14	US-10-232-175-17	Sequence 17, Appl
26	132	100.0	1487	15	US-10-342-331-48	Sequence 48, Appl
27	132	100.0	1487	15	US-10-342-331-50	Sequence 50, Appl
28	132	100.0	1487	15	US-10-342-331-49	Sequence 49, Appl
29	132	100.0	1487	15	US-10-901-816A-5	Sequence 5, Appli
30	132	100.0	1487	17	US-10-901-816A-6	Sequence 6, Appli
31	132	100.0	1487	17	US-10-901-816A-7	Sequence 7, Appli
32	132	100.0	1487	17	US-10-901-816A-8	Sequence 8, Appli
33	132	100.0	1487	17	US-10-901-816A-9	Sequence 9, Appli
34	132	100.0	1487	17	US-10-901-816A-10	Sequence 10, Appl
35	132	100.0	1487	17	US-10-901-816A-11	Sequence 11, Appl
36	132	100.0	1487	17	US-10-901-816A-13	Sequence 13, Appl
37	132	100.0	1487	15	US-10-104-889-16	Sequence 16, Appl
38	132	100.0	1487	15	US-10-104-889-20	Sequence 20, Appl
39	132	100.0	1487	18	US-10-104-793-16	Sequence 16, Appl
40	132	100.0	1487	18	US-10-104-793-20	Sequence 20, Appl
41	132	100.0	1487	15	US-10-104-889-11	Sequence 11, Appl
42	132	100.0	1487	18	US-10-104-793-11	Sequence 11, Appl
43	132	100.0	1487	15	US-10-104-889-6	Sequence 6, Appli
44	132	100.0	1487	18	US-10-104-793-6	Sequence 6, Appli
45	132	100.0	1487	15	US-10-104-889-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-10-674-065-3
; Sequence 3, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-674-065-3

Query Match 100.0%; Score 132; DB 16; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.2e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGQAGFGPGTGLPGVK 23
DB 1 ERGPPGQAGFGPGTGLPGVK 23

RESULT 2

```

US-10-674-065-6
; Sequence 6, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 6
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (15)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (18)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (21)
; OTHER INFORMATION: hydroxylated proline
; OTHER INFORMATION: hydroxylated proline
; SEQ ID NO 7
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: hydroxylated proline
; NAME/KEY: MOD_RES
; LOCATION: (18)
; OTHER INFORMATION: hydroxylated proline
; OTHER INFORMATION: hydroxylated proline
; NAME/KEY: MOD_RES
; LOCATION: (18)

Query Match 100.0%; Score 132; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGLPGVK 23
Db 2 ERGPPGPGQARGPFGTGLPGVK 24

RESULT 3
US-10-674-065-7
; Sequence 7, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: hydroxylated proline
; NAME/KEY: MOD_RES
; LOCATION: (15)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (21)
; OTHER INFORMATION: hydroxylated proline
; OTHER INFORMATION: hydroxylated proline
; SEQ ID NO 8
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (15)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (21)
; OTHER INFORMATION: hydroxylated proline
; OTHER INFORMATION: hydroxylated proline
; SEQ ID NO 9
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: hydroxylated proline
; NAME/KEY: MOD_RES
; LOCATION: (18)

```

```

; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (21)
; OTHER INFORMATION: hydroxylated proline
US-10-674-065-7
Query Match 100.0%; Score 132; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGLPGVK 23
Db 2 ERGPPGPGQARGPFGTGLPGVK 24

RESULT 4
US-10-674-065-8
; Sequence 8, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 8
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (15)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (21)
; OTHER INFORMATION: hydroxylated proline
; OTHER INFORMATION: hydroxylated proline
; SEQ ID NO 9
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (15)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (21)
; OTHER INFORMATION: hydroxylated proline
; OTHER INFORMATION: hydroxylated proline
; SEQ ID NO 10
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: hydroxylated proline
; NAME/KEY: MOD_RES
; LOCATION: (18)

```

```

; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (21)
; OTHER INFORMATION: hydroxylated proline
US-10-674-065-8
Query Match 100.0%; Score 132; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 7.4e-08;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGLPGVK 23
Db 2 ERGPPGPGQARGPFGTGLPGVK 24

RESULT 5
US-10-674-065-9
; Sequence 9, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332

```

;
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 24
; TYPE: PRT

;
; ORGANISM: Artificial Sequence

;
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide

;
; FEATURE:

;
; NAME/KEY: MOD_RES

;
; LOCATION: (6)
; OTHER INFORMATION: hydroxylated proline

;
; FEATURE:

;
; NAME/KEY: MOD_RES

;
; LOCATION: (15)
; OTHER INFORMATION: hydroxylated proline

;
; FEATURE:

;
; NAME/KEY: MOD_RES

;
; LOCATION: (18)
; OTHER INFORMATION: hydroxylated proline

;
; OTHER INFORMATION: hydroxylated proline

US-10-674-065-9

Query Match 100.0%; Score 132; DB 16; Length 24;

Best Local Similarity 100.0%; Pred. No. 7.4e-08;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGQARGPFGTGLPGVK 23

DB 2 ERGPPGQARGPFGTGLPGVK 24

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

;
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SAME
; FILE REFERENCE: 079328-0105

;
; CURRENT APPLICATION NUMBER: US/10/674,065

;
; CURRENT FILING DATE: 2003-09-30

;
; PRIOR APPLICATION NUMBER: 60/414,332

;
; PRIOR FILING DATE: 2002-09-30

;
; NUMBER OF SEQ ID NOS: 18

;
; SOFTWARE: PatentIn Ver. 3.2

;
; SEQ ID NO 14

;
; LENGTH: 24

;
; TYPE: PRT

;
; ORGANISM: Artificial Sequence

;
; FEATURE:

;
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

;
; OTHER INFORMATION: peptide

;
; FEATURE:

;
; NAME/KEY: MOD_RES

;
; LOCATION: (6)

;
; OTHER INFORMATION: hydroxylated proline

;
; FEATURE:

;
; NAME/KEY: MOD_RES

;
; LOCATION: (15)

;
; OTHER INFORMATION: hydroxylated proline

;
; FEATURE:

;
; NAME/KEY: MOD_RES

;
; LOCATION: (18)

;
; OTHER INFORMATION: hydroxylated proline

;
; FEATURE:

;
; NAME/KEY: MOD_RES

;
; LOCATION: (21)

;
; OTHER INFORMATION: hydroxylated proline

;
; OTHER INFORMATION: hydroxylated proline

US-10-674-065-14

Query Match 100.0%; Score 132; DB 16; Length 24;

Best Local Similarity 100.0%; Pred. No. 7.4e-08;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGQARGPFGTGLPGVK 23

DB 2 ERGPPGQARGPFGTGLPGVK 24

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

;
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SAME
; FILE REFERENCE: 079328-0105

;
; CURRENT APPLICATION NUMBER: US/10/674,065

;
; CURRENT FILING DATE: 2003-09-30

;
; PRIOR APPLICATION NUMBER: 60/414,332

;
; PRIOR FILING DATE: 2002-09-30

;
; NUMBER OF SEQ ID NOS: 18

;
; SOFTWARE: PatentIn Ver. 3.2

;
; SEQ ID NO 9

;
; LENGTH: 24

;
; TYPE: PRT

;
; ORGANISM: Artificial Sequence

;
; FEATURE:

;
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

;
; OTHER INFORMATION: peptide

;
; FEATURE:

;
; NAME/KEY: MOD_RES

;
; LOCATION: (6)

;
; OTHER INFORMATION: hydroxylated proline

;
; FEATURE:

;
; NAME/KEY: MOD_RES

;
; LOCATION: (15)

;
; OTHER INFORMATION: hydroxylated proline

;
; FEATURE:

;
; NAME/KEY: MOD_RES

;
; LOCATION: (18)

;
; OTHER INFORMATION: hydroxylated proline

;
; FEATURE:

;
; NAME/KEY: MOD_RES

;
; LOCATION: (21)

;
; OTHER INFORMATION: hydroxylated proline

;
; OTHER INFORMATION: hydroxylated proline

US-10-674-065-14

Query Match 100.0%; Score 132; DB 16; Length 24;

Best Local Similarity 100.0%; Pred. No. 7.4e-08;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGQARGPFGTGLPGVK 23

DB 2 ERGPPGQARGPFGTGLPGVK 24

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

;
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SAME
; FILE REFERENCE: 079328-0105

;
; CURRENT APPLICATION NUMBER: US/10/674,065

;
; CURRENT FILING DATE: 2003-09-30

;
; PRIOR APPLICATION NUMBER: 60/414,332

;
; PRIOR FILING DATE: 2002-09-30

;
; NUMBER OF SEQ ID NOS: 18

;
; SOFTWARE: PatentIn Ver. 3.2

;
; SEQ ID NO 9

;
; LENGTH: 24

;
; TYPE: PRT

;
; ORGANISM: Artificial Sequence

;
; FEATURE:

;
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic

;
; OTHER INFORMATION: peptide

;
; FEATURE:

;
; NAME/KEY: MOD_RES

;
; LOCATION: (6)

;
; OTHER INFORMATION: hydroxylated proline

;
; FEATURE:

;
; NAME/KEY: MOD_RES

;
; LOCATION: (15)

;
; OTHER INFORMATION: hydroxylated proline

;
; FEATURE:

;
; NAME/KEY: MOD_RES

;
; LOCATION: (18)

;
; OTHER INFORMATION: hydroxylated proline

;
; FEATURE:

;
; NAME/KEY: MOD_RES

;
; LOCATION: (21)

;
; OTHER INFORMATION: hydroxylated proline

;
; OTHER INFORMATION: hydroxylated proline

US-10-674-065-14

Query Match 100.0%; Score 132; DB 16; Length 24;

Best Local Similarity 100.0%; Pred. No. 7.4e-08;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGQARGPFGTGLPGVK 23

DB 2 ERGPPGQARGPFGTGLPGVK 24

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

|||||

;
; TITLE OF INVENTION: METHODS FOR IDENTIFYING SAME
; FILE REFERENCE: 079328-0105

```
RESULT 9
US-10-674-065-18
; Sequence 18, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; METHODS FOR IDENTIFYING SAME
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 18
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (12)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (21)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (30)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (39)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (42)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (45)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (54)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (66)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (75)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (81)
; OTHER INFORMATION: hydroxylated proline
; OTHER INFORMATION: hydroxylated proline
US-10-674-065-18
```

```
Query Match      100.0%; Score 132; DB 16; Length 84;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ERGPPGPGQARGFPCTGGLPGVK 23
      |||||
Db      26 ERGPPGPGQARGFPCTGGLPGVK 48
      |||||

RESULT 10
US-10-674-065-11
; Sequence 11, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; METHODS FOR IDENTIFYING SAME
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 11
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; OTHER INFORMATION: hydroxylated proline
US-10-674-065-11
```

```
Query Match      100.0%; Score 132; DB 16; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ERGPPGPGQARGFPCTGGLPGVK 23
      |||||
Db      26 ERGPPGPGQARGFPCTGGLPGVK 48
      |||||

RESULT 11
US-10-674-065-12
; Sequence 12, Application US/10674065
; Publication No. US20040122209A1
; GENERAL INFORMATION:
; APPLICANT: POOLE, A. ROBIN
; TITLE OF INVENTION: PRODUCTS FOR REGULATING THE DEGRADATION OF COLLAGEN AND
; METHODS FOR IDENTIFYING SAME
; FILE REFERENCE: 079328-0105
; CURRENT APPLICATION NUMBER: US/10/674,065
; CURRENT FILING DATE: 2003-09-30
; PRIOR APPLICATION NUMBER: 60/414,332
; PRIOR FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 12
; LENGTH: 85
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (6)
; OTHER INFORMATION: hydroxylated proline
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (9)
; OTHER INFORMATION: hydroxylated proline
; OTHER INFORMATION: hydroxylated proline
US-10-674-065-12
```


FEATURE:
NAME/KEY: MOD RES
LOCATION: (12)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (21)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (30)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (39)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (42)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (45)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (66)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (75)
OTHER INFORMATION: hydroxylated proline
FEATURE:
NAME/KEY: MOD RES
LOCATION: (81)
OTHER INFORMATION: hydroxylated proline
US-10-674-065-12

Query Match 100.0%; Score 132; DB 16; Length 85;
Best Local Similarity 100.0%; Pred. No. 2.3e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGLPGVK 23
Db 26 ERGPPGPGQARGPFGTGLPGVK 48

RESULT 12
US-10-723-860-1085
Sequence 1085, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION:
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions &
TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators
FILE REFERENCE: 05882.0193.NPUS01
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8393
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1085
LENGTH: 243
TYPE: PRT
ORGANISM: Homo sapiens
US-10-723-860-1085

Query Match 100.0%; Score 132; DB 16; Length 243;
Best Local Similarity 100.0%; Pred. No. 6e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGLPGVK 23
Db 167 ERGPPGPGQARGPFGTGLPGVK 189

RESULT 13
US-10-639-286-11
Sequence 11, Application US/10639286
Publication No. US20040115217A1
GENERAL INFORMATION:
APPLICANT: Weiner, Howard
APPLICANT: Miller, Ariel
APPLICANT: Zheng, Zhengyi
APPLICANT: Ahmad, Al-Sabbagh
TITLE OF INVENTION: BYSTANDER SUPPRESSION OF AUTOIMMUNE DISEASE
FILE REFERENCE: 01010/1006959-US7
CURRENT APPLICATION NUMBER: US/10/639,286
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: US 08/472,017
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 07/843,752
PRIOR FILING DATE: 1992-02-28
PRIOR APPLICATION NUMBER: US 07/460,852
PRIOR FILING DATE: 1990-02-21
PRIOR APPLICATION NUMBER: US 07/596,936
PRIOR FILING DATE: 1990-10-15
PRIOR APPLICATION NUMBER: US 07/065,734
PRIOR FILING DATE: 1987-06-24
PRIOR APPLICATION NUMBER: US 07/454,486
PRIOR FILING DATE: 1989-12-20
PRIOR APPLICATION NUMBER: US 07/487,732
PRIOR FILING DATE: 1990-03-02
PRIOR APPLICATION NUMBER: US 07/551,632
PRIOR FILING DATE: 1990-07-10
PRIOR APPLICATION NUMBER: US 07/379,778
PRIOR FILING DATE: 1989-07-14
PRIOR APPLICATION NUMBER: US 07/607,826
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 492
TYPE: PRT
ORGANISM: Bos taurus
US-10-639-286-11

Query Match 100.0%; Score 132; DB 16; Length 492;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ERGPPGPGQARGPFGTGLPGVK 23
Db 65 ERGPPGPGQARGPFGTGLPGVK 87

RESULT 14
US-10-194-441A-1
Sequence 1, Application US/10194441A
Publication No. US20030148944A1
GENERAL INFORMATION:
APPLICANT: Holmdahl, Rikard
APPLICANT: Engstrom, Jan Ake
APPLICANT: Kihlberg, Jan
APPLICANT: Burkhardt, Harald
TITLE OF INVENTION: TRIPLE POLYPEPTIDE COMPLEXES
FILE REFERENCE: 11145-010001
CURRENT APPLICATION NUMBER: US/10/194,441A
CURRENT FILING DATE: 2002-07-11
PRIOR APPLICATION NUMBER: US 60/305,048
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 87

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1014
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-194-441A-1

Query Match      100.0%; Score 132; DB 14; Length 1014;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ERGPPGPGQARGPPTGTLPGVK 23
DB      65 ERGPPGPGQARGPPTGTLPGVK 87

RESULT 15
US-10-639-286-10
; Sequence 10, Application US/10639286
; Publication No. US20040115217A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, Howard
; APPLICANT: Miller, Ariel
; APPLICANT: Zheng, Zhengyi
; TITLE OF INVENTION: BYSTANDER SUPPRESSION OF AUTOIMMUNE DISEASE
; FILE REFERENCE: 01010/1006959-US7
; CURRENT APPLICATION NUMBER: US/10/639,286
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: US 08/472,017
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 07/843,752
; PRIOR FILING DATE: 1992-02-28
; PRIOR APPLICATION NUMBER: US 07/460,852
; PRIOR FILING DATE: 1990-02-21
; PRIOR APPLICATION NUMBER: US 07/596,936
; PRIOR FILING DATE: 1990-10-15
; PRIOR APPLICATION NUMBER: US 07/065,734
; PRIOR FILING DATE: 1987-06-24
; PRIOR APPLICATION NUMBER: US 07/454,486
; PRIOR FILING DATE: 1989-12-20
; PRIOR APPLICATION NUMBER: US 07/487,732
; PRIOR FILING DATE: 1990-03-02
; PRIOR APPLICATION NUMBER: US 07/551,632
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: US 07/379,778
; PRIOR FILING DATE: 1989-07-14
; PRIOR APPLICATION NUMBER: US 07/607,826
; PRIOR FILING DATE: 1990-10-31
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1017
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-639-286-10

Query Match      100.0%; Score 132; DB 16; Length 1017;
Best Local Similarity 100.0%; Pred. No. 2.2e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ERGPPGPGQARGPPTGTLPGVK 23
DB      65 ERGPPGPGQARGPPTGTLPGVK 87

```

Search completed: October 8, 2005, 00:30:14
Job time : 167 secs